

## SEQUENCE LISTING

<110> University of Utah Research Foundation  
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<120> Omega-Conopeptides

<130> 2314-241

<150> US 60/219,616

<151> 2000-07-21

<150> US 60/265,888

<151> 2001-02-05

<160> 413

<170> PatentIn version 3.0

<210> 1

<211> 318

<212> DNA

<213> Unknown

<220>

<223> unknown Conus species

<400> 1

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 aatttctcca cgttgactcg tcgctgcctt tctcccgat cacgatgtca taagacaatg 180  
 cgtaactgct gcaattcatg ctcttcatac aaagggaaat gtcggcctcg aaaatgaacc 240  
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<210> 2

<211> 76

<212> PRT

<213> Unknown

<220>

<223> unknown Conus species

<400> 2

Met Lys Leu Thr Cys Met Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His His  
 20 25 30

Ala Leu Arg Ser Thr Thr Asn Phe Ser Thr Leu Thr Arg Arg Cys Leu  
 35 40 45

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Ser Pro Gly Ser Arg Cys His Lys Thr Met Arg Asn Cys Cys Thr Ser  
50 55 60

Cys Ser Ser Tyr Lys Gly Lys Cys Arg Pro Arg Lys  
65 70 75

<210> 3  
<211> 30  
<212> PRT  
<213> Unknown

<220>  
<223> unknown Conus species

<220>  
<221> PEPTIDE  
<222> (1)..(30)  
<223> Xaa at residue 4 and 28 is Pro or Hyp; Xaa at residue 22 is Tyr,  
125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-T  
y

<400> 3  
Cys Leu Ser Xaa Gly Ser Arg Cys His Lys Thr Met Arg Asn Cys Cys  
1 5 10 15

Thr Ser Cys Ser Ser Xaa Lys Gly Lys Cys Arg Xaa Arg Lys  
20 25 30

<210> 4  
<211> 283  
<212> DNA  
<213> Unknown

<220>  
<223> unknown Conus species

<400> 4  
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ctcatcacag ctgatgactc cagaggtacg cagaagcatt atgccctgag gtcgaccacc 120  
aattttctcca cgtcgactcg tcgctgcaaa cctcccggaa gaaaatgtct gaatagaaag 180  
aatgaatgct gcagcaagtt ttgcaatgaa cacctacata tgtgtggata aatggctaaa 240  
aactgaataa aagccgcatt gcaaaaaaaaa aaaaaaaaaa aaa 283

<210> 5  
<211> 74  
<212> PRT  
<213> Unknown

<220>  
<223> unknown Conus species

<400> 5  
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1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His His  
20 25 30

Ala Leu Arg Ser Thr Thr Asn Phe Ser Thr Ser Thr Arg Arg Cys Lys  
35 40 45

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Pro Pro Gly Arg Lys Cys Leu Asn Arg Lys Asn Glu Cys Cys Ser Lys  
50 55 60

Phe Cys Asn Glu His Leu His Met Cys Gly  
65 70

<210> 6  
<211> 27  
<212> PRT  
<213> Unknown

<220>  
<223> unknown Conus species

<220>  
<221> PEPTIDE  
<222> (1)..(27)  
<223> Xaa at residue 14 and 22 is Glu or gamma-carboxy Glu; Xaa at resi  
due 3 and 4 is Pro or Hy

<400> 6  
Cys Lys Xaa Xaa Gly Arg Lys Cys Leu Asn Arg Lys Asn Xaa Cys Cys  
1 5 10 15

Ser Lys Phe Cys Asn Xaa His Leu His Met Cys  
20 25

<210> 7  
<211> 275  
<212> DNA  
<213> Unknown

<220>  
<223> unknown Conus species

<400> 7  
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ctcgtcacag ctgatggctc cagaggtatg cagaagcatt atgccctgag gtcgaccacc 120  
aatctctcca tatcgtctcg ctgcaaacct cccagaagaa aatgtctgaa gattaaggat 180  
aaatgctgca actttttgcaa tacacaccta aatatgtgtg gataaatggc taaaaactga 240  
ataaaagccg cattgcaaaa aaaaaaaaaa aaaaa 275

<210> 8  
<211> 72  
<212> PRT  
<213> Unknown

<220>  
<223> unknown Conus species

<400> 8  
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
1 5 10 15

Cys Gln Leu Val Thr Ala Asp Gly Ser Arg Gly Met Gln Lys His Tyr  
20 25 30

Ala Leu Arg Ser Thr Thr Asn Leu Ser Ile Ser Ser Arg Cys Lys Pro  
35 40 45

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Pro Arg Arg Lys Cys Leu Lys Ile Lys Asp Lys Cys Cys Asn Phe Cys  
50 55 60

Asn Thr His Leu Asn Met Cys Gly  
65 70

<210> 9  
<211> 26  
<212> PRT  
<213> Unknown

<220>  
<223> unknown Conus species

<220>  
<221> PEPTIDE  
<222> (1)..(26)  
<223> Xaa at residue 3 and 4 is Pro or Hyp

<400> 9  
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1 5 10 15

Asn Phe Cys Asn Thr His Leu Asn Met Cys  
20 25

<210> 10  
<211> 377  
<212> DNA  
<213> Unknown

<220>  
<223> unknown Conus species

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aaactctcca tgtcgactcg ctgcgcaggt ccaggaacaa tttgtcctaa taggggatgc 180  
tgcggttatt gcagtaaaaag aacacatcta tgtcattcgc gaactggctg atcttcccc 240  
ttctgcgctc catccttttc tgcttgagtc ctccatacct gagaatggctc atgaaccact 300  
caacacctac tcctctggag ggcctcagaa gagctacatt gaaataaaaag ccgcattaca 360  
aaaaaaaaa aaaaaaa 377

<210> 11  
<211> 74  
<212> PRT  
<213> Unknown

<220>  
<223> unknown Conus species

<400> 11  
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Met Ala  
1 5 10 15

Cys Gln Leu Val Thr Ala Asp Gly Ser Arg Gly Met His Lys His Tyr  
20 25 30

Ala Leu Arg Ser Thr Thr Lys Leu Ser Met Ser Thr Arg Cys Ala Gly

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35 40 45  
 Pro Gly Thr Ile Cys Pro Asn Arg Val Cys Cys Gly Tyr Cys Ser Lys  
 50 55 60

Arg Thr His Leu Cys His Ser Arg Thr Gly  
 65 70

<210> 12  
 <211> 28  
 <212> PRT  
 <213> Unknown

<220>  
 <223> unknown Conus species

<220>  
 <221> PEPTIDE  
 <222> (1)..(28)  
 <223> Xaa at residue 4 and 9 is Pro or Hyp; Xaa at residue 16 is Tyr, 1  
 25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 12  
 Cys Ala Gly Xaa Gly Thr Ile Cys Xaa Asn Arg Val Cys Cys Gly Xaa  
 1 5 10 15

Cys Ser Lys Arg Thr His Leu Cys His Ser Arg Thr  
 20 25

<210> 13  
 <211> 323  
 <212> DNA  
 <213> Conus arenatus

<400> 13  
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 ctcattacag gtgagcagaa ggaccatgct ctgagggtcaa ctgacaaaaa ctccaagttg 120  
 actaggcagt gctcggctaa cgggtggatct tgtactcgtc attttcactg ctgcagcctc 180  
 tattgcaata aagattccag tgtatgtgtg gcaacctcat acccgtgagt ggccatgaac 240  
 ccctcaatac cctctcctct ggaggcttca gaggaactgc attgaaataa aaccgcattg 300  
 caataaaaaa aaaaaaaaaa aaa 323

<210> 14  
 <211> 73  
 <212> PRT  
 <213> Conus arenatus

<400> 14  
 Met Lys Leu Thr Cys Met Val Ile Ile Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Gly Glu Gln Lys Asp His Ala Leu Arg Ser Thr  
 20 25 30

Asp Lys Asn Ser Lys Leu Thr Arg Gln Cys Ser Ala Asn Gly Gly Ser  
 35 40 45

Cys Thr Arg His Phe His Cys Cys Ser Leu Tyr Cys Asn Lys Asp Ser  
 50 55 60

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Ser Val Cys Val Ala Thr Ser Tyr Pro  
65 70

<210> 15  
<211> 33  
<212> PRT  
<213> Conus arenatus

<220>  
<221> PEPTIDE  
<222> (1)..(33)  
<223> Xaa at residue 1 is Gn or pyro-Glu; Xaa at residue 33 is Pro or H  
yp; Xaa at residue 19 and 32 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-  
iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 15

Xaa Cys Ser Ala Asn Gly Gly Ser Cys Thr Arg His Phe His Cys Cys  
1 5 10 15

Ser Leu Xaa Cys Asn Lys Asp Ser Ser Val Cys Val Ala Thr Ser Xaa  
20 25 30

Xaa

<210> 16  
<211> 326  
<212> DNA  
<213> Conus arenatus

<400> 16

accaaaacca tcatcaaaat gaaactgacg tgcgtgttga ttatcgccgt gctgttcctg 60  
acggcctgtc aactcattac agctgagact tactccagag gtgagcagaa gcaccatgct 120  
ctgaggtcaa ctgacagaaa ctccaagttg accaggacat gcaacactcc cactgaatat 180  
tgtactttgc atcgacactg ctgcagcggc tactgccata aaacaatcca ggcattgttca 240  
taataccggt gagtggatcat gaaccactca ataccctctc ctctggagggc ttcagaggaa 300  
ctgcattgaa ataaaagccg cattgc 326

<210> 17  
<211> 74  
<212> PRT  
<213> Conus arenatus

<400> 17

Met Lys Leu Thr Cys Val Leu Ile Ile Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Cys Gln Leu Ile Thr Ala Glu Thr Tyr Ser Arg Gly Glu Gln Lys His  
20 25 30

His Ala Leu Arg Ser Thr Asp Arg Asn Ser Lys Leu Thr Arg Thr Cys  
35 40 45

Asn Thr Pro Thr Glu Tyr Cys Thr Leu His Arg His Cys Cys Ser Gly  
50 55 60

Tyr Cys His Lys Thr Ile Gln Ala Cys Ser  
65 70

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<210> 18  
 <211> 28  
 <212> PRT  
 <213> Conus arenatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(28)  
 <223> Xaa at residue 7 is Glu or gamma-carboxy Glu; Xaa at residue 5 is Pro or Hyp; Xaa at residue 8 and 19 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 18  
 Thr Cys Asn Thr Xaa Thr Xaa Xaa Cys Thr Leu His Arg His Cys Cys  
 1 5 10 15

Ser Gly Xaa Cys His Lys Thr Ile Gln Ala Cys Ser  
 20 25

<210> 19  
 <211> 332  
 <212> DNA  
 <213> Conus arenatus

<400> 19  
 accaaaacca tcatcaaaat gaaactgacg tgcgtgttga tcatcgccgt gctgttcctg 60  
 acggcctgtc aactcattac agctgagact tactccagag gtgagcagat gcaccgtgct 120  
 ctgaggtcaa ctgacaaaaa ctccaagttg actaggcagt gcacgcctaa cggtggatct 180  
 tgttctcgtc attttcactg ctgcagcctc tattgcaata aaagtactgg cgtatgtatt 240  
 gcaacctcat acccgtgagt ggtcatgaac cactcaatac cctctcctct ggaggcttca 300  
 gaggaactgc attgaaataa aagccgcatt gc 332

<210> 20  
 <211> 79  
 <212> PRT  
 <213> Conus arenatus

<400> 20  
 Met Lys Leu Thr Cys Val Leu Ile Ile Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Glu Thr Tyr Ser Arg Gly Glu Gln Met His  
 20 25 30

Arg Ala Leu Arg Ser Thr Asp Lys Asn Ser Lys Leu Thr Arg Gln Cys  
 35 40 45

Thr Pro Asn Gly Gly Ser Cys Ser Arg His Phe His Cys Cys Ser Leu  
 50 55 60

Tyr Cys Asn Lys Ser Thr Gly Val Cys Ile Ala Thr Ser Tyr Pro  
 65 70 75

<210> 21  
 <211> 33  
 <212> PRT  
 <213> Conus arenatus

<220>  
 <221> PEPTIDE

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<222> (1)..(33)  
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 4 and 33 is P  
 ro or Hyp; Xaa at residue 19 and 32 is Tyr, 125I-Tyr, mono-iodo-T  
 yr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 21  
 Xaa Cys Thr Xaa Asn Gly Gly Ser Cys Ser Arg His Phe His Cys Cys  
 1 5 10 15  
 Ser Leu Xaa Cys Asn Lys Ser Thr Gly Val Cys Ile Ala Thr Ser Xaa  
 20 25 30  
 Xaa

<210> 22  
 <211> 332  
 <212> DNA  
 <213> Conus arenatus

<400> 22  
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 ctccattacag ctgagactta ctccagaggt gagcagaagc accatgctct gaggtcaact 120  
 gacaaaaact ccaagttgac caggacatgc aacactccca ccgaatattg tactttgcat 180  
 caaacactgct gcagcggcta ctgccataaa acaatccagg catgttcata ataccggtga 240  
 gtggtcatga accactcaat accctctcct ctggaggcct cagaggaact gcattgaaat 300  
 aaaaccgcat tacaaaaaaaa aaaaaaaaaa aa 332

<210> 23  
 <211> 74  
 <212> PRT  
 <213> Conus arenatus

<400> 23  
 Met Lys Leu Thr Cys Met Val Ile Ile Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15  
 Cys Gln Leu Ile Thr Ala Glu Thr Tyr Ser Arg Gly Glu Gln Lys His  
 20 25 30  
 His Ala Leu Arg Ser Thr Asp Lys Asn Ser Lys Leu Thr Arg Thr Cys  
 35 40 45  
 Asn Thr Pro Thr Glu Tyr Cys Thr Leu His Gln His Cys Cys Ser Gly  
 50 55 60  
 Tyr Cys His Lys Thr Ile Gln Ala Cys Ser  
 65 70

<210> 24  
 <211> 28  
 <212> PRT  
 <213> Conus arenatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(28)  
 <223> Xaa at residue 7 is Glu or gamma-carboxy Glu; Xaa at residue 5 is  
 Pro or Hyp; Xaa at residue 8 and 19 is Tyr, 125I-Tyr, mono-iodo-  
 Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

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<400> 24  
 Thr Cys Asn Thr Xaa Thr Xaa Xaa Cys Thr Leu His Gln His Cys Cys  
 1 5 10 15

Ser Gly Xaa Cys His Lys Thr Ile Gln Ala Cys Ser  
 20 25

<210> 25  
 <211> 394  
 <212> DNA  
 <213> Conus arenatus

<400> 25  
 ggatccatga aactgacgtg tatggtgata atcgccgtac tgttcctgac ggcctgtcaa 60

ctcattacag ctgagactta ctccagaggt aagcagatgc accgcgctct gaggtcaact 120

gacaaaaact ccagttgac cagggaatgc acacctcccg gtggagcttg tggtttacct 180

acacactgct gcgggttttg cgatactgca aacaacagat gtctgtaaaag ctggtctggc 240

gtctgatatt ccccttctgt gctctatcct ctttggcctg agtcatccgt acctgtgagt 300

ggatcatgaac tactcaatac cctctcctct ggaggcttca gaggaactac aatgaaataa 360

aaccgcgatt gcagagaaaa aaaaaaaaaa aaaa 394

<210> 26  
 <211> 73  
 <212> PRT  
 <213> Conus arenatus

<400> 26  
 Met Lys Leu Thr Cys Met Val Ile Ile Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Glu Thr Tyr Ser Arg Gly Lys Gln Met His  
 20 25 30

Arg Ala Leu Arg Ser Thr Asp Lys Asn Ser Gln Leu Thr Arg Glu Cys  
 35 40 45

Thr Pro Pro Gly Gly Ala Cys Gly Leu Pro Thr His Cys Cys Gly Phe  
 50 55 60

Cys Asp Thr Ala Asn Asn Arg Cys Leu  
 65 70

<210> 27  
 <211> 27  
 <212> PRT  
 <213> Conus arenatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(27)  
 <223> Xaa at residue 1 is Glu or gamma-carboxy Glu; Xaa at residue 4, 5  
 and 12 is Pro or Hy

<400> 27  
 Xaa Cys Thr Xaa Xaa Gly Gly Ala Cys Gly Leu Xaa Thr His Cys Cys  
 1 5 10 15

Gly Phe Cys Asp Thr Ala Asn Asn Arg Cys Leu

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20

25

<210> 28  
 <211> 345  
 <212> DNA  
 <213> Conus arenatus

<220>  
 <221> misc\_feature  
 <222> (1)..(345)  
 <223> n may be any nucleotide

<400> 28  
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 ctccattacag ctgagactta ctccagaggt gagcagaatc accatgttct gaggtcaact 120  
 gacaaaaact ccaagttgac caggacatgc aacactccca ctgaatattg tactttgcat 180  
 caacactgct gcagcggcca ctgccataaa acaatccagg catgtgcata ataccggtgg 240  
 gtggtcatga accactcaat accctctcct ctggaggctt cagaggaact gcattgaaat 300  
 aaaaccgcat tgcaatgaan aaaaaaaaaa aaaaaaaaaa aaaaaa 345

<210> 29  
 <211> 74  
 <212> PRT  
 <213> Conus arenatus

<400> 29  
 Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15  
 Cys Gln Leu Ile Thr Ala Glu Thr Tyr Ser Arg Gly Glu Gln Asn His  
 20 25 30  
 His Val Leu Arg Ser Thr Asp Lys Asn Ser Lys Leu Thr Arg Thr Cys  
 35 40 45  
 Asn Thr Pro Thr Glu Tyr Cys Thr Leu His Gln His Cys Cys Ser Gly  
 50 55 60  
 His Cys His Lys Thr Ile Gln Ala Cys Ala  
 65 70

<210> 30  
 <211> 28  
 <212> PRT  
 <213> Conus arenatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(28)  
 <223> Xaa at residue 7 is Glu or gamma-carboxy Glu; Xaa at residue 5 is  
 Pro or Hyp; Xaa at residue 8 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-  
 iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 30  
 Thr Cys Asn Thr Xaa Thr Xaa Xaa Cys Thr Leu His Gln His Cys Cys  
 1 5 10 15  
 Ser Gly His Cys His Lys Thr Ile Gln Ala Cys Ala  
 20 25

09910082.072301

<210> 31  
 <211> 322  
 <212> DNA  
 <213> Conus arenatus

<400> 31  
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 ctactacag gtgagcagaa ggaccatgct ctgaggtcaa ctgacaaaaa ctccaagttg 120  
 actaggcagt gctgcctat cgggtggatat tgtactcttc atattcactg ctgcagcaac 180  
 cattgcatta aacctatcgg ccgatgtgtg gcaacctgat acccgtgcgt ggtcatgaac 240  
 ccctcaatac cctctcctct ggaggcttca gaggaactgc attgaaataa aaccgcattg 300

caataaaaaa aaaaaaaaaa aa

322

<210> 32  
 <211> 70  
 <212> PRT  
 <213> Conus arenatus

<400> 32  
 Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15  
 Cys Gln Leu Thr Thr Gly Glu Gln Lys Asp His Ala Leu Arg Ser Thr  
 20 25 30  
 Asp Lys Asn Ser Lys Leu Thr Arg Gln Cys Ser Pro Ile Gly Gly Tyr  
 35 40 45  
 Cys Thr Leu His Ile His Cys Cys Ser Asn His Cys Ile Lys Pro Ile  
 50 55 60  
 Gly Arg Cys Val Ala Thr  
 65 70

<210> 33  
 <211> 30  
 <212> PRT  
 <213> Conus arenatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(30)  
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 4 and 23 is P  
 ro or Hyp; Xaa at residue 8 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-i  
 odo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 33  
 Xaa Cys Ser Xaa Ile Gly Gly Xaa Cys Thr Leu His Ile His Cys Cys  
 1 5 10 15  
 Ser Asn His Cys Ile Lys Xaa Ile Gly Arg Cys Val Ala Thr  
 20 25 30

<210> 34  
 <211> 318  
 <212> DNA  
 <213> Conus arenatus

<400> 34  
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 actaggcagt gcttgcctaa cggtggatat tgtactcttc atattcactg ctgcagcgac 180  
 cattgcatta aacctatcga ccgatgtgtg gcaacctgat acccgggcgt ggtcatgaac 240  
 ccctcaatac cctctcctct ggaggcttca gaggaactgc attgaaataa aaccgcatta 300  
 caaaaaaaaa aaaaaaaaa 318

<210> 35  
 <211> 70  
 <212> PRT  
 <213> Conus arenatus

<400> 35  
 Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15  
 Cys Gln Leu Thr Thr Gly Glu Gln Lys Asp His Ala Leu Arg Ser Thr  
 20 25 30  
 Asp Lys Asn Ser Lys Leu Thr Arg Gln Cys Leu Pro Asn Gly Gly Tyr  
 35 40 45  
 Cys Thr Leu His Ile His Cys Cys Ser Asp His Cys Ile Lys Pro Ile  
 50 55 60  
 Asp Arg Cys Val Ala Thr  
 65 70

<210> 36  
 <211> 30  
 <212> PRT  
 <213> Conus arenatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(30)  
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 4 and 23 is P  
 ro or Hyp; Xaa at residue 8 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-i  
 odo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 36  
 Xaa Cys Leu Xaa Asn Gly Gly Xaa Cys Thr Leu His Ile His Cys Cys  
 1 5 10 15  
 Ser Asp His Cys Ile Lys Xaa Ile Asp Arg Cys Val Ala Thr  
 20 25 30

<210> 37  
 <211> 374  
 <212> DNA  
 <213> Conus aurisiacus

<400> 37  
 atgaaactga cgtgtgtggt gatcgtcgcc gtgctgctcc tgacggcctg tcaactcatc 60  
 acagctgatg actccagagg tacgcagaag catcggtccc tgagctcggc caccaaactc 120  
 tccatgtcga ctgctgcaa gggtaaagga aaaccatgca gtaggatttc gtataactgc 180  
 tgcaccggtt cttgcagatc aggtaaatgt ggctgatcca gcgcctgatc ttcccccttc 240

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tgtgctctat ccttttctgc ctgagtcctc cttacctgag agtgggtcatg aaccactcat 300  
cacctgctcc tctggaggcc ccagaggagc tacattgaaa taaaagtcgc attgcaaaaa 360  
aaaaaaaaaa aaaa 374

<210> 38  
<211> 71  
<212> PRT  
<213> Conus aurisiacus

<400> 38  
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
20 25 30

Ser Leu Ser Ser Ala Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Gly  
35 40 45

Lys Gly Lys Pro Cys Ser Arg Ile Ser Tyr Asn Cys Cys Thr Gly Ser  
50 55 60

Cys Arg Ser Gly Lys Cys Gly  
65 70

<210> 39  
<211> 25  
<212> PRT  
<213> Conus aurisiacus

<220>  
<221> PEPTIDE  
<222> (1)..(25)  
<223> Xaa at residue 7 is Pro or Hyp; Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 39  
Cys Lys Gly Lys Gly Lys Xaa Cys Ser Arg Ile Ser Xaa Asn Cys Cys  
1 5 10 15

Thr Gly Ser Cys Arg Ser Gly Lys Cys  
20 25

<210> 40  
<211> 380  
<212> DNA  
<213> Conus aurisiacus

<400> 40  
atgaaactga cgtgtgtggt gatcgctgcc gtgctgctcc tgacggcctg tcaactcatc 60  
acagctgatg actccagagg tacgcagaag catcggtccc tgaggctgaa gaccaaactc 120  
tccatgtcga ctggctgcat ggaagccgga tcttattgcg gctctactac gagaatctgc 180  
tgcggttttt gcgcttattt cggcaaaaaa tgtattgact atcccagcaa ctgatcttcc 240  
ccctactgtg ctctatcctt ttctgcctga gtctcctta cctgagagtg gtcataaacc 300  
actcatcacc tgctcctctg gaggccccag aggagctaca ttgaaataaa atcgcatcgc 360  
taaaaaaaaaa aaaaaaaaaa 380

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<210> 41  
 <211> 77  
 <212> PRT  
 <213> Conus aurisiacus

<400> 41  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15  
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30  
 Ser Leu Arg Ser Lys Thr Lys Leu Ser Met Ser Thr Gly Cys Met Glu  
 35 40 45  
 Ala Gly Ser Tyr Cys Gly Ser Thr Thr Arg Ile Cys Cys Gly Phe Cys  
 50 55 60

Ala Tyr Phe Gly Lys Lys Cys Ile Asp Tyr Pro Ser Asn  
 65 70 75

<210> 42  
 <211> 32  
 <212> PRT  
 <213> Conus aurisiacus

<220>  
 <221> PEPTIDE  
 <222> (1)..(32)  
 <223> Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 30 is  
 s Pro or Hyp; Xaa at residue 7, 21 and 29 is Tyr, 125I-Tyr, mono-  
 iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 42  
 Cys Met Xaa Ala Gly Ser Xaa Cys Gly Ser Thr Thr Arg Ile Cys Cys  
 1 5 10 15  
 Gly Phe Cys Ala Xaa Phe Gly Lys Lys Cys Ile Asp Xaa Xaa Ser Asn  
 20 25 30

<210> 43  
 <211> 373  
 <212> DNA  
 <213> Conus aurisiacus

<400> 43  
 accaaaacca tcatcaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60  
 acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgttcctg 120  
 agctcggcca ccaaactctc catgtcgact cgctgcaagg cttaaaggaaa accatgcagt 180  
 aggattgcgt ataactgctg caccggttct tgcagatcag gtaaagtgtg ctgatccagt 240  
 gcctgatctt ccccttctg tgcctatcc ttttctgcct gagtcctcct tacctgagag 300  
 tggatcatgaa ccaatcatca cctgctcctc tggaggcccc agaggagcta cattgaaata 360  
 aaagccgcat tgc 373

<210> 44  
 <211> 71  
 <212> PRT  
 <213> Conus aurisiacus

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&lt;400&gt; 44

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
20 25 30

Ser Leu Ser Ser Ala Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Ala  
35 40 45

Lys Gly Lys Pro Cys Ser Arg Ile Ala Tyr Asn Cys Cys Thr Gly Ser  
50 55 60

Cys Arg Ser Gly Lys Cys Gly  
65 70

&lt;210&gt; 45

&lt;211&gt; 25

&lt;212&gt; PRT

&lt;213&gt; Conus aurisiacus

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(25)

<223> Xaa at residue 7 is Pro or Hyp; Xaa at residue 13 is Tyr, 125I-Tyr,  
r, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

&lt;400&gt; 45

Cys Lys Ala Lys Gly Lys Xaa Cys Ser Arg Ile Ala Xaa Asn Cys Cys  
1 5 10 15

Thr Gly Ser Cys Arg Ser Gly Lys Cys  
20 25

&lt;210&gt; 46

&lt;211&gt; 379

&lt;212&gt; DNA

&lt;213&gt; Conus aurisiacus

&lt;400&gt; 46

accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60

acgacctgtc aactcatcac agctgatgac tccagaggta cgcaggagca tcgtgccctg 120

aggtcgaaga caaaactctc catgttaact ttgcgctgcg catcttacgg aaaaccttgt 180

ggtattgaca acgactgctg caatgcatgc gatccaggaa gaaatatatg tacgtagctg 240

atccagcgcc tgatcttccc cttctgtgc tctatccttt tctgcccagag tctccttac 300

ctgagagtgg tcatgaacca ctcatcacct gctccctgga ggctcagag gagctacaat 360

gaaataaaaag ccgcattgc 379

&lt;210&gt; 47

&lt;211&gt; 72

&lt;212&gt; PRT

&lt;213&gt; Conus aurisiacus

&lt;400&gt; 47

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Thr  
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Glu His Arg  
20 25 30

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Ala Leu Arg Ser Lys Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Ala  
35 40 45

Ser Tyr Gly Lys Pro Cys Gly Ile Asp Asn Asp Cys Cys Asn Ala Cys  
50 55 60

Asp Pro Gly Arg Asn Ile Cys Thr  
65 70

<210> 48  
<211> 26  
<212> PRT  
<213> Conus aurisiacus

<220>  
<221> PEPTIDE  
<222> (1)..(26)  
<223> Xaa at residue 7 and 20 is Pro or Hyp; Xaa at residue 4 is Tyr, 1  
25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 48  
Cys Ala Ser Xaa Gly Lys Xaa Cys Gly Ile Asp Asn Asp Cys Cys Asn  
1 5 10 15

Ala Cys Asp Xaa Gly Arg Asn Ile Cys Thr  
20 25

<210> 49  
<211> 382  
<212> DNA  
<213> Conus bullatus

<400> 49  
accaaaacca tcatcaaaat gaaactgacg tgtgtggcga tcgtcgccgt gctgctcctg 60  
acggcctgtc agctcattac agctgaagac tccagaggta cgcattgagca tcttgccctg 120  
aagtcgacct ccaaagtctc caagtcgact agctgcatgg aagccggatc ttattgcgga 180  
cctgtacta cgaaaatctg ctgcatgttt tgcagtccat tcagcgatag atgtatgaac 240  
aatcccaaca attgatcttc ccccttggtg gctccatcct tttctgcctg agtcctcctt 300  
acctgagagt ggtcatgaac cactcatcac ctactcctct ggaggcttca gaggagctac 360  
attgaaataa aagccgcatt gc 382

<210> 50  
<211> 78  
<212> PRT  
<213> Conus bullatus

<400> 50  
Met Lys Leu Thr Cys Val Ala Ile Val Ala Val Leu Leu Leu Thr Ala  
1 5 10 15

Cys Gln Leu Ile Thr Ala Glu Asp Ser Arg Gly Thr His Glu His Leu  
20 25 30

Ala Leu Lys Ser Thr Ser Lys Val Ser Lys Ser Thr Ser Cys Met Glu  
35 40 45

Ala Gly Ser Tyr Cys Gly Pro Ala Thr Thr Lys Ile Cys Cys Asp Phe

00100807230



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<400>      53
Met  Lys  Leu  Thr  Cys  Val  Val  Ile  Val  Ala  Val  Leu  Leu  Leu  Thr  Ala
 1                                     10                               15

Cys  Gln  Leu  Ile  Thr  Ala  Glu  Asp  Ser  Arg  Gly  Thr  Gln  Leu  His  Arg
          20                                     25                               30

Ala  Leu  Arg  Lys  Ala  Thr  Lys  His  Pro  Val  Ser  Thr  Arg  Cys  Ile  Thr
          35                                     40                               45

Pro  Gly  Thr  Arg  Cys  Lys  Val  Pro  Ser  Gln  Cys  Cys  Arg  Gly  Pro  Cys
      50          55          60

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Lys Asn Gly Arg Cys Thr Pro Ser Pro Ser Glu Trp  
65 70 75

<210> 54  
<211> 31  
<212> PRT  
<213> Conus bullatus

<220>  
<221> PEPTIDE  
<222> (1)..(31)  
<223> Xaa at residue 30 is Glu or gamma-carboxy Glu; Xaa at residue 4,  
11, 18, 26 and 28 is Pro or Hyp; Xaa at residue 31 is Trp or Bromo  
Tr

<400> 54

Cys Ile Thr Xaa Gly Thr Ala Cys Lys Val Xaa Ser Gln Cys Cys Arg  
1 5 10 15

Gly Xaa Cys Lys Asn Gly Arg Cys Thr Xaa Ser Xaa Ser Xaa Xaa  
20 25 30

<210> 55  
<211> 379  
<212> DNA  
<213> Conus bullatus

<400> 55

accataaacca tcatcaaaat gaaactgacg tgtgtggcga tcgtgcgcgt gctgctcctg 60  
acggcctgtc agctcattac agctgaggac tccagagata cgcagaagca tcgtgcctctg 120  
aggtcggaca ccaaactctc catgttgact ttgcgctgcg caacttacgg aaaaccttgt 180  
ggtattcaaa acgactgctg caatacatgc gatccagcca gaaggacatg tacgtagctg 240  
atccggcgctc ttgatcctcc gcttctgtgc tccatctttt ctgcctgagt cctccttacc 300  
tgagagtggg catgaaccac tcatcaccta ctctcttgga ggctttagag gagctacatt 360  
gaaataaaag ccgcattgc 379

<210> 56  
<211> 72  
<212> PRT  
<213> Conus bullatus

<400> 56

Met Lys Leu Thr Cys Val Ala Ile Val Ala Val Leu Leu Leu Thr Ala  
1 5 10 15

Cys Gln Leu Ile Thr Ala Glu Asp Ser Arg Asp Thr Gln Lys His Arg  
20 25 30

Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Ala  
35 40 45

Thr Tyr Gly Lys Pro Cys Gly Ile Gln Asn Asp Cys Cys Asn Thr Cys  
50 55 60

Asp Pro Ala Arg Arg Thr Cys Thr  
65 70

<210> 57  
<211> 26

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<212> PRT  
<213> Conus bullatus

<220>  
<221> PEPTIDE  
<222> (1)..(26)  
<223> Xaa at residue 7 and 20 is Pro or Hyp; Xaa at residue 4 is Tyr, 1  
25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 57  
Cys Ala Thr Xaa Gly Lys Xaa Cys Gly Ile Gln Asn Asp Cys Cys Asn  
1 5 10 15  
Thr Cys Asp Xaa Ala Arg Arg Thr Cys Thr  
20 25

<210> 58  
<211> 373  
<212> DNA  
<213> Conus bullatus  
  
<400> 58  
accaaaacca tcatcaaaat gaaactgacg tgtgtggcga tcgtcgccgt gctgctcctg 60  
acggcctgtc agctcattac agctgaagac tccagaggta cgcagttgca tcgtgccctg 120  
aggaagacca ccaaactctc cttgtcgact cgctgcaagg gtccaggagc atcatgtata 180  
aggattgcgt ataactgctg caagtattct tgcagaaatg gtaaagtgtg ctgatccagc 240  
gcctgatctt ccccttctgt tgcctccatcc tttctctgcct gagtcctcct tacctgagag 300  
tggtcatgaa ccactcatca cctactcctc tggaggcttc agaggagcta cattgaaata 360  
aaagccgcat tgc 373

<210> 59  
<211> 71  
<212> PRT  
<213> Conus bullatus

<400> 59  
Met Lys Leu Thr Cys Val Ala Ile Val Ala Val Leu Leu Leu Thr Ala  
1 5 10 15  
Cys Gln Leu Ile Thr Ala Glu Asp Ser Arg Gly Thr Gln Leu His Arg  
20 25 30  
Ala Leu Arg Lys Thr Thr Lys Leu Ser Leu Ser Thr Arg Cys Lys Gly  
35 40 45  
Pro Gly Ala Ser Cys Ile Arg Ile Ala Tyr Asn Cys Cys Lys Tyr Ser  
50 55 60  
Cys Arg Asn Gly Lys Cys Gly  
65 70

<210> 60  
<211> 25  
<212> PRT  
<213> Conus bullatus

<220>  
<221> PEPTIDE

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<222> (1)..(25)  
 <223> Xaa at residue 4 is Pro or Hyp; Xaa at residue 13 and 18 is Tyr,  
 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-T  
 y

<400> 60  
 Cys Lys Gly Xaa Gly Ala Ser Cys Ile Arg Ile Ala Xaa Asn Cys Cys  
 1 5 10 15  
 Lys Xaa Ser Cys Arg Asn Gly Lys Cys  
 20 25

<210> 61  
 <211> 382  
 <212> DNA  
 <213> *Conus bullatus*

<400> 61  
 atcaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60  
 acggcctgtc agctcattac agctgaagac tccagaggta cgcattgagca tcttgccctg 120  
 aagtcgacct ccaaagtctc caagtcgact agctgcatgg cagccggatc ttattgcgga 180  
 cctgtacta cgaatatctg ctgcgatttt tgcagtccat tcagcgatag atgtatgaaa 240  
 aagcccaaca attgatcttc ccccttctgt gctctatcct tttctgcctg agtcctcctt 300  
 acctgagagt ggcatgaac cactcatcac ctactcctct ggaggcttca gaggagctac 360  
 attgaaataa aagccgcatt gc 382

<210> 62  
 <211> 78  
 <212> PRT  
 <213> *Conus bullatus*

<400> 62  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15  
 Cys Gln Leu Ile Thr Ala Glu Asp Ser Arg Gly Thr His Glu His Leu  
 20 25 30  
 Ala Leu Lys Ser Thr Ser Lys Val Ser Lys Ser Thr Ser Cys Met Ala  
 35 40 45  
 Ala Gly Ser Tyr Cys Gly Pro Ala Thr Thr Asn Ile Cys Cys Asp Phe  
 50 55 60  
 Cys Ser Pro Phe Ser Asp Arg Cys Met Lys Lys Pro Asn Asn  
 65 70 75

<210> 63  
 <211> 36  
 <212> PRT  
 <213> *Conus bullatus*

<220>  
 <221> PEPTIDE  
 <222> (1)..(36)  
 <223> Xaa at residue 13, 25 and 34 is Pro or Hyp; Xaa at residue 10 is  
 Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phos  
 pho-Ty

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<400> 63  
 Ser Thr Ser Cys Met Ala Ala Gly Ser Xaa Cys Gly Xaa Ala Thr Thr  
 1 5 10 15

Asn Ile Cys Cys Asp Phe Cys Ser Xaa Phe Ser Asp Arg Cys Met Lys  
 20 25 30

Lys Xaa Asn Asn  
 35

<210> 64  
 <211> 373  
 <212> DNA  
 <213> Conus bullatus

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<400> 64  
 accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60  
 acggcctgtc agctcattat agctgaggac tccagaggta cgcagttgca tcgtgccctg 120  
 aggaaggcca ccaaactctc cgtgtcgact cgctgcaaga gtaaaggatc atcatgtcat 180  
 aggacttcgt atgactgctg cacgggttct tgcagaaatg gtagatgtgg ctgatccagc 240  
 gcctgatctt ccccttctg tgctccatcc ttttctgcct gagtcctcct tacctgagag 300  
 tggtcatgaa ccaactcatca cctactcctc tggaggcttc agaggagcta cattgaaata 360  
 aaagccgcat tgc 373

<210> 65  
 <211> 71  
 <212> PRT  
 <213> Conus bullatus

<400> 65  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15  
 Cys Gln Leu Ile Ile Ala Glu Asp Ser Arg Gly Thr Gln Leu His Arg  
 20 25 30  
 Ala Leu Arg Lys Ala Thr Lys Leu Ser Val Ser Thr Arg Cys Lys Ser  
 35 40 45  
 Lys Gly Ser Ser Cys His Arg Thr Ser Tyr Asp Cys Cys Thr Gly Ser  
 50 55 60  
 Cys Arg Asn Gly Arg Cys Gly  
 65 70

<210> 66  
 <211> 25  
 <212> PRT  
 <213> Conus bullatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(25)  
 <223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O  
 -sulpho-Tyr or O-phospho-Ty

<400> 66  
 Cys Lys Ser Lys Gly Ser Ser Cys His Arg Thr Ser Xaa Asp Cys Cys  
 1 5 10 15

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Thr Gly Ser Cys Arg Asn Gly Arg Cys  
20 25

<210> 67  
<211> 321  
<212> DNA  
<213> Conus characteristicus

<400> 67  
ggatccatga aactgacgtg cgtggtgatc atcgccgtgc tgttcctgac ggccctgtcaa 60  
ctcattacag gtgagcagaa ggaccatgct ctgagggtcaa ctgacaaaaa ctccaagttg 120  
actaggcagt gctcggctaa cgggtggatct tgtactcgtc attttcactg ctgcagcctc 180  
tattgcaata aagattccag tgtatgtgtg gcaacctcat acccgtgagt ggccatgaac 240  
ccctcaatac cctctcctct ggaggcttca gaggaactgc attgaaataa aaccgcatta 300  
caaaaaaaaaa aaaaaaaaaa a 321

<210> 68  
<211> 73  
<212> PRT  
<213> Conus characteristicus

<400> 68  
Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala  
1 5 10 15  
Cys Gln Leu Ile Thr Gly Glu Gln Lys Asp His Ala Leu Arg Ser Thr  
20 25 30  
Asp Lys Asn Ser Lys Leu Thr Arg Gln Cys Ser Ala Asn Gly Gly Ser  
35 40 45  
Cys Thr Arg His Phe His Cys Cys Ser Leu Tyr Cys Asn Lys Asp Ser  
50 55 60  
Ser Val Cys Val Ala Thr Ser Tyr Pro  
65 70

<210> 69  
<211> 33  
<212> PRT  
<213> Conus characteristicus

<220>  
<221> PEPTIDE  
<222> (1)..(33)  
<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 33 is Pro or Hyp; Xaa at residue 19 and 32 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 69  
Xaa Cys Ser Ala Asn Gly Gly Ser Cys Thr Arg His Phe His Cys Cys  
1 5 10 15  
Ser Leu Xaa Cys Asn Lys Asp Ser Ser Val Cys Val Ala Thr Ser Xaa  
20 25 30

Xaa

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<210> 70  
 <211> 26  
 <212> PRT  
 <213> Conus catus

<400> 70  
 Cys Lys Ser Thr Gly Ala Ser Cys Arg Arg Thr Ser Tyr Asp Cys Cys  
 1 5 10 15  
 Thr Gly Ser Cys Arg Ser Gly Arg Cys Gly  
 20 25

<210> 71  
 <211> 25  
 <212> PRT  
 <213> Conus catus

<220>  
 <221> PEPTIDE  
 <222> (1)..(25)  
 <223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 71  
 Cys Lys Ser Thr Gly Ala Ser Cys Arg Arg Thr Ser Xaa Asp Cys Cys  
 1 5 10 15  
 Thr Gly Ser Cys Arg Ser Gly Arg Cys  
 20 25

<210> 72  
 <211> 229  
 <212> DNA  
 <213> Conus catus

<400> 72  
 tcgactcgct gccagggtag aggagcatca tgtcgtaaga ctatgtataa ctgctgcagc 60  
 gggtctttgca acagaggtag ttgtggctga tccggcgccct gatcttcccc cttccgtgct 120  
 ctatcctttt ctgcctgatt cctccttacc tgagagcgggt catgaaccac tcatcacctg 180  
 ctcctctgga ggcctcagag gagctacatt gaaataaaag ccgcattgc 229

<210> 73  
 <211> 29  
 <212> PRT  
 <213> Conus catus

<400> 73  
 Ser Thr Arg Cys Gln Gly Arg Gly Ala Ser Cys Arg Lys Thr Met Tyr  
 1 5 10 15  
 Asn Cys Cys Ser Gly Ser Cys Asn Arg Gly Ser Cys Gly  
 20 25

<210> 74  
 <211> 25  
 <212> PRT  
 <213> Conus catus

<220>  
 <221> PEPTIDE  
 <222> (1)..(25)  
 <223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O

-sulpho-Tyr or O-phospho-Ty

<400> 74

Cys Gln Gly Arg Gly Ala Ser Cys Arg Lys Thr Met Xaa Asn Cys Cys  
1 5 10 15

Ser Gly Ser Cys Asn Arg Gly Ser Cys  
20 25

<210> 75

<211> 235

<212> DNA

<213> Conus catus

<400> 75

tcgacacgct gcttgctgc cggagagtct tgccttttta gtaggattag atgctgcggt 60

acttgcagtt cagtcttaaa gtcattgtgtg agctgatcca gctgctgac ttctctctcc 120

tgtgctccat ccttttctgc ctgagtcctc cttatctgag agtggtcatg aaccactcac 180

cacctactct tctggaggct tcagaggagc tacagtgaat taaaagccgc attgc 235

<210> 76

<211> 31

<212> PRT

<213> Conus catus

<400> 76

Ser Thr Arg Cys Leu Pro Ala Gly Glu Ser Cys Leu Phe Ser Arg Ile  
1 5 10 15

Arg Cys Cys Gly Thr Cys Ser Ser Val Leu Lys Ser Cys Val Ser  
20 25 30

<210> 77

<211> 28

<212> PRT

<213> Conus catus

<220>

<221> PEPTIDE

<222> (1)..(28)

<223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 3 is Pro or Hy

<400> 77

Cys Leu Xaa Ala Gly Xaa Ser Cys Leu Phe Ser Arg Ile Arg Cys Cys  
1 5 10 15

Gly Thr Cys Ser Ser Val Leu Lys Ser Cys Val Ser  
20 25

<210> 78

<211> 227

<212> DNA

<213> Conus catus

<400> 78

tcgacacgct gccagggtag aggaggacca tgtactaagg ctgtgtttta ctgctgcagc 60

ggttcttgca acagaggtag atgtggctga tccagcgct gatcttcccc cttctgtgct 120

ctatcctttt ctgcctgagt cctccttact gagagtagtc atgaaccaact catcacctac 180

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tcctctggag gcctcagaga gctacattga aataaaagcc gcattgc

227

<210> 79  
 <211> 29  
 <212> PRT  
 <213> Conus catus

<400> 79  
 Ser Thr Arg Cys Gln Gly Arg Gly Gly Pro Cys Thr Lys Ala Val Phe  
 1 5 10 15

Asn Cys Cys Ser Gly Ser Cys Asn Arg Gly Arg Cys Gly  
 20 25

<210> 80  
 <211> 25  
 <212> PRT  
 <213> Conus catus

<220>  
 <221> PEPTIDE  
 <222> (1)..(25)  
 <223> Xaa at residue 7 is Pro or Hyp

<400> 80  
 Cys Gln Gly Arg Gly Gly Xaa Cys Thr Lys Ala Val Phe Asn Cys Cys  
 1 5 10 15

Ser Gly Ser Cys Asn Arg Gly Arg Cys  
 20 25

<210> 81  
 <211> 236  
 <212> DNA  
 <213> Conus catus

<400> 81  
 ttaactttgc gctgcgcaac ttacggaaaa ccttggtgta ttcaaaacga ctgctgcaat 60  
 acatgcatc cagccagaaa gacatgtacg tagctgatcc ggcgtctgat ctccccctt 120  
 ctgtgctcta tccttttctg cctgagtcct ccttacctga gagggtcat gaaccactca 180  
 tcacctgctc ctctggaggc ctcgggggag ctacattgaa ataaaagccg cattgc 236

<210> 82  
 <211> 30  
 <212> PRT  
 <213> Conus catus

<400> 82  
 Leu Thr Leu Arg Cys Ala Thr Tyr Gly Lys Pro Cys Gly Ile Gln Asn  
 1 5 10 15

Asp Cys Cys Asn Thr Cys Asp Pro Ala Arg Lys Thr Cys Thr  
 20 25 30

<210> 83  
 <211> 26  
 <212> PRT  
 <213> Conus catus

<220>  
 <221> PEPTIDE

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<222> (1)..(26)  
 <223> Xaa at residue 7 and 20 is Pro or Hyp; Xaa at residue 4 is Tyr, 1  
 25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 83  
 Cys Ala Thr Xaa Gly Lys Xaa Cys Gly Ile Gln Asn Asp Cys Cys Asn  
 1 5 10 15  
 Thr Cys Asp Xaa Ala Arg Lys Thr Cys Thr  
 20 25

<210> 84  
 <211> 229  
 <212> DNA  
 <213> Conus catus

<400> 84  
 tcgactcgct gccggggtag aggaggacca tgtactaagg ctatgtttaa ctgctgcagc 60  
 ggttccttgca acagaggttag atgtggctga tccagcgcct gatcttcccc cttctgtgct 120  
 ctatcctttt ctgcctgagt cctccttaac tgagagtagt catgaaccac tcatcaccta 180  
 ctctctgga ggcctcagag aagcatcatt gaaataaaaag ccgcattgc 229

<210> 85  
 <211> 29  
 <212> PRT  
 <213> Conus catus

<400> 85  
 Ser Thr Arg Cys Arg Gly Arg Gly Gly Pro Cys Thr Lys Ala Met Phe  
 1 5 10 15  
 Asn Cys Cys Ser Gly Ser Cys Asn Arg Gly Arg Cys Gly  
 20 25

<210> 86  
 <211> 25  
 <212> PRT  
 <213> Conus catus

<220>  
 <221> PEPTIDE  
 <222> (1)..(25)  
 <223> Xaa at residue 7 is Pro or Hyp

<400> 86  
 Cys Arg Gly Arg Gly Gly Xaa Cys Thr Lys Ala Met Phe Asn Cys Cys  
 1 5 10 15  
 Ser Gly Ser Cys Asn Arg Gly Arg Cys  
 20 25

<210> 87  
 <211> 374  
 <212> DNA  
 <213> Conus circumcisis

<400> 87  
 accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60  
 acgacctgtc aactcatcac agctgatgac tccagaggta cgcaggagca tcgtgcctg 120

0910082.072901

aggctcggaca ccaaactccc catgtcgact cgctgcaagg gtaaaggagc atcatgtcgt 180  
aagactatgt ataactgctg cagcggttct tgcagcaacg gtagatgtgg ctgatccagc 240  
gcctgatctt ccccttctg ctgctctatc cttttctgcc tgagtcctcc ttacctgaga 300  
gctgggtcatg aaccactcat cacctgctcc tctggaggcc cagaggagct acattgaaat 360  
aaaagccgca ttgc 374

<210> 88  
<211> 71  
<212> PRT  
<213> Conus circumcisis

~~<400> 88~~

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Thr  
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Glu His Arg  
20 25 30

Ala Leu Arg Ser Asp Thr Lys Leu Pro Met Ser Thr Arg Cys Lys Gly  
35 40 45

Lys Gly Ala Ser Cys Arg Lys Thr Met Tyr Asn Cys Cys Ser Gly Ser  
50 55 60

Cys Ser Asn Gly Arg Cys Gly  
65 70

<210> 89  
<211> 25  
<212> PRT  
<213> Conus circumcisis

<220>  
<221> PEPTIDE  
<222> (1)..(25)  
<223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 89  
Cys Lys Gly Lys Gly Ala Ser Cys Arg Lys Thr Met Xaa Asn Cys Cys  
1 5 10 15

Ser Gly Ser Cys Ser Asn Gly Arg Cys  
20 25

<210> 90  
<211> 379  
<212> DNA  
<213> Conus circumcisis

<400> 90  
acaaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60  
acgacctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccctg 120  
aggctcggcca ccaaagtctc caagtcgact agctgcatgg aagccggatc ttattgccgc 180  
tctactacga gaacctgctg cggttattgc tcttatttca gcaaaaaatg tattgacttt 240  
cccagcaact gatcttcccc ctactgtgct ctatcctttt ctgcctgagt cctccttacc 300

09910082.072301

tgagagtggt catgaaccac tcatcacct actcctctgg aggcccagag gagctacatt 360  
gaaataaaaag ccgcattgc 379

<210> 91  
<211> 77  
<212> PRT  
<213> Conus circumciscus

<400> 91  
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Thr  
1 5 10 15  
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
20 25 30

Ala Leu Arg Ser Ala Thr Lys Val Ser Lys Ser Thr Ser Cys Met Glu  
35 40 45

Ala Gly Ser Tyr Cys Arg Ser Thr Thr Arg Thr Cys Cys Gly Tyr Cys  
50 55 60

Ser Tyr Phe Ser Lys Lys Cys Ile Asp Phe Pro Ser Asn  
65 70 75

<210> 92  
<211> 35  
<212> PRT  
<213> Conus circumciscus

<220>  
<221> PEPTIDE  
<222> (1)..(35)  
<223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 33 is  
Pro or Hyp; Xaa at residue 10, 21 and 24 is Tyr, 125I-Tyr, mono-  
iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 92  
Ser Thr Ser Cys Met Xaa Ala Gly Ser Xaa Cys Arg Ser Thr Thr Arg  
1 5 10 15

Thr Cys Cys Gly Xaa Cys Ser Xaa Phe Ser Lys Lys Cys Ile Asp Phe  
20 25 30

Xaa Ser Asn  
35

<210> 93  
<211> 379  
<212> DNA  
<213> Conus circumciscus

<400> 93  
accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60  
acgacctgtc aactcatcac agctgatgac tccagaggta cgcaggagca tcgtgccctg 120  
aggtcggaca ccaaactccc catgtcgact cgctgcaaga gtaaaggagc aaaatgttca 180  
aggcttatgt atgactgctg cagcggttct tgcagcaggt actcaggtag atgtggctga 240  
tccagcgcct gatcttcccc cttctgctgc tctatccttt tctgcctgag tcttccttac 300  
ctgagagtgg tcatgaacca tcatcacct actcctctgg aggcccagag gagctacatt 360

09910082.072304

gaaataaaaag ccgcattgc

379

&lt;210&gt; 94

&lt;211&gt; 73

&lt;212&gt; PRT

&lt;213&gt; Conus circumciscus

&lt;400&gt; 94

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Thr  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Glu His Arg  
 20 25 30

Ala Leu Arg Ser Asp Thr Lys Leu Pro Met Ser Thr Arg Cys Lys Ser  
 35 40 45

Lys Gly Ala Lys Cys Ser Arg Leu Met Tyr Asp Cys Cys Ser Gly Ser  
 50 55 60

Cys Ser Arg Tyr Ser Gly Arg Cys Gly  
 65 70

&lt;210&gt; 95

&lt;211&gt; 27

&lt;212&gt; PRT

&lt;213&gt; Conus circumciscus

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(27)

<223> Xaa at residue 13 and 23 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

&lt;400&gt; 95

Cys Lys Ser Lys Gly Ala Lys Cys Ser Arg Leu Met Xaa Asp Cys Cys  
 1 5 10 15

Ser Gly Ser Cys Ser Arg Xaa Ser Gly Arg Cys  
 20 25

&lt;210&gt; 96

&lt;211&gt; 379

&lt;212&gt; DNA

&lt;213&gt; Conus circumciscus

&lt;400&gt; 96

accaaaacca tcataaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60

acgacctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgttccttg 120

acgtcggcca ccaaagtctc caagtcgact ggctgcatga aagccggatc ttattgccgc 180

tctactacga gaacttgctg cggttattgc gcttatttcg gcaaaaaatg tattgactat 240

cccagcaact gatcttcccc ctactgtgct ctatcctttt ctgcctaagt cctccttacc 300

tgagagtggc catgaaccac tcatcaccct actcctctgg aggcccagag gagctacatt 360

gaaataaaaag ccgcattgc 379

&lt;210&gt; 97

&lt;211&gt; 77

&lt;212&gt; PRT

&lt;213&gt; Conus circumciscus

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&lt;400&gt; 97

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Thr  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30

Ser Leu Thr Ser Ala Thr Lys Val Ser Lys Ser Thr Gly Cys Met Lys  
 35 40 45

Ala Gly Ser Tyr Cys Arg Ser Thr Thr Arg Thr Cys Cys Gly Tyr Cys  
 50 55 60

Ala Tyr Phe Gly Lys Lys Cys Ile Asp Tyr Pro Ser Asn  
 65 70 75

&lt;210&gt; 98

&lt;211&gt; 35

&lt;212&gt; PRT

&lt;213&gt; Conus circumciscus

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(35)

<223> Xaa at residue 33 is Pro or Hyp; Xaa at residue 10, 21, 24 and 32  
 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-  
 phospho-Ty

&lt;400&gt; 98

Ser Thr Gly Cys Met Lys Ala Gly Ser Xaa Cys Arg Ser Thr Thr Arg  
 1 5 10 15

Thr Cys Cys Gly Xaa Cys Ala Xaa Phe Gly Lys Lys Cys Ile Asp Xaa  
 20 25 30

Xaa Ser Asn  
 35

&lt;210&gt; 99

&lt;211&gt; 362

&lt;212&gt; DNA

&lt;213&gt; Conus consors

&lt;400&gt; 99

atgaaactga cgtgtgtggt gatcgtcgcc gtgctgctcc tgacggcctg tcaactcctc 60  
 acagctgatg actccagagg tacgcagaag catcgtgccc tgaagtotta caccaaactc 120  
 tccatgttaa ctttgcgctg cgcattcttac ggaaaacctt gtggtattga caacgactgc 180  
 tgcaatacat gcgatccagc cagaaagaca tgtacgtagc tgatccggcg tctgatcttc 240  
 ccccttctgt gctctatcct tttctgcctg agtcctcctt acctgagagt ggtcatgaac 300  
 cactcatcac ctagctcctc tggaggcttc agaggagcta caatgaaata aaagcgcatt 360  
 gc 362

&lt;210&gt; 100

&lt;211&gt; 72

&lt;212&gt; PRT

&lt;213&gt; Conus consors

&lt;400&gt; 100

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Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
1 5 10 15

Cys Gln Leu Leu Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
20 25 30

Ala Leu Lys Ser Tyr Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Ala  
35 40 45

Ser Tyr Gly Lys Pro Cys Gly Ile Asp Asn Asp Cys Cys Asn Thr Cys  
50 55 60

Asp Pro Ala Arg Lys Thr Cys Thr  
65 70

<210> 101

<211> 26

<212> PRT

<213> Conus consors

<220>

<221> PEPTIDE

<222> (1)..(26)

<223> Xaa at residue 7 and 20 is Pro or Hyp; Xaa at residue 4 is Tyr, 1  
25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 101

Cys Ala Ser Xaa Gly Lys Xaa Cys Gly Ile Asp Asn Asp Cys Cys Asn  
1 5 10 15

Thr Cys Asp Xaa Ala Arg Lys Thr Cys Thr  
20 25

<210> 102

<211> 237

<212> DNA

<213> Conus consors

<400> 102

atgaaactga cgtgtgtggt gatcgctgcc gtgctgctcc tgacggcctg tcaactcctc 60

acagctgatg actccagagg tacgcagaag catcgtgccc tgaggtcgga caccaaactc 120

tccatgtcga ctcgctgcaa gggtacagga aaaccatgca gtaggattgc gtataactgc 180

tgcaaccggtt cttgcagatc aggtaaatgt ggctgatcca gcgcctgac tcccccc 237

<210> 103

<211> 71

<212> PRT

<213> Conus consors

<400> 103

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
1 5 10 15

Cys Gln Leu Leu Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
20 25 30

Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Gly  
35 40 45

Thr Gly Lys Pro Cys Ser Arg Ile Ala Tyr Asn Cys Cys Thr Gly Ser  
50 55 60

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Cys Arg Ser Gly Lys Cys Gly  
65 70

<210> 104  
<211> 25  
<212> PRT  
<213> Conus consors

<220>  
<221> PEPTIDE  
<222> (1)..(25)  
<223> Xaa at residue 7 is Pro or Hyp; Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 104

Cys Lys Gly Arg Gly Lys Xaa Cys Ser Arg Ile Ala Xaa Asn Cys Cys  
1 5 10 15

Thr Gly Ser Cys Arg Ser Gly Lys Cys  
20 25

<210> 105  
<211> 320  
<212> DNA  
<213> Conus consors

<400> 105

atgaaactga cgtgtgtggt gatcgctgcc gtgctgctcc tgacggcctg tcaactcatc 60  
acagctgatg actccaaagg tacgcagaag catcggtccc tgaggctcgac caccaaagtc 120  
tccaaggcga ctgactgcat tgaagccgga aattattgcg gacctactgt tatgaaaatc 180  
tgctgctggct tttgcagtcc atacagcaaa atatgtatga actatcccca aaattgatct 240  
tcccccttct gtgctctatc cttttctgcc tgagtcctcc ttacctgaga gtggatcatga 300  
accactcatc acctcgtccc 320

<210> 106  
<211> 78  
<212> PRT  
<213> Conus consors

<400> 106

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Lys Gly Thr Gln Lys His Arg  
20 25 30

Ser Leu Arg Ser Thr Thr Lys Val Ser Lys Ala Thr Asp Cys Ile Glu  
35 40 45

Ala Gly Asn Tyr Cys Gly Pro Thr Val Met Lys Ile Cys Cys Gly Phe  
50 55 60

Cys Ser Pro Tyr Ser Lys Ile Cys Met Asn Tyr Pro Gln Asn  
65 70 75

<210> 107  
<211> 36  
<212> PRT  
<213> Conus consors

09910082.072301



<220>  
 <221> PEPTIDE  
 <222> (1)..(36)  
 <223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 13, 25 and 34 is Pro or Hyp; Xaa at residue 10, 26 and 33 is Tyr, 125 I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 107  
 Ala Thr Asp Cys Ile Xaa Ala Gly Asn Xaa Cys Gly Xaa Thr Val Met  
 1 5 10 15  
 Lys Ile Cys Cys Gly Phe Cys Ser Xaa Xaa Ser Lys Ile Cys Met Asn  
 20 25 30  
 Xaa Xaa Gln Asn  
 35

<210> 108  
 <211> 321  
 <212> DNA  
 <213> Conus consors  
 <400> 108  
 atgaaactga cgtgtgtggt gatcgtcgcc gtgctgctcc tgacggcctg tcaactcctc 60  
 acagctgatg actccagagg tacgcagaag catcgtgccc tgaggtcgga caccaaactc 120  
 tccatgtcga ctgctgcaa aggtaaagga gcatcatgta caaggcttat gtatgactgc 180  
 tgccacgggt cttgcagcag cagcaagggt agatgtggct gatccggcgc ctgatcttcc 240  
 cccttctgtg ctctatcctt ttctgctga gtctctctta cctgagaggt ggtcatgaac 300  
 cactcatcac ctgctcccct g 321

<210> 109  
 <211> 73  
 <212> PRT  
 <213> Conus consors

<400> 109  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15  
 Cys Gln Leu Leu Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30  
 Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Gly  
 35 40 45  
 Lys Gly Ala Ser Cys Thr Arg Leu Met Tyr Asp Cys Cys His Gly Ser  
 50 55 60  
 Cys Ser Ser Ser Lys Gly Arg Cys Gly  
 65 70

<210> 110  
 <211> 27  
 <212> PRT  
 <213> Conus consors

<220>  
 <221> PEPTIDE

0010082-07301  
 100220-28001660

<222> (1)..(27)  
 <223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 110  
 Cys Lys Gly Lys Gly Ala Ser Cys Thr Arg Leu Met Xaa Asp Cys Cys  
 1 5 10 15

His Gly Ser Cys Ser Ser Ser Lys Gly Arg Cys  
 20 25

<210> 111  
 <211> 292  
 <212> DNA  
 <213> Conus consors

<400> 111  
 ggatccatga aactgacgtg catggtgata gtcgccgtgc tgctcctgac ggcctgtcaa 60  
 ctcatcacag ctgatgactc cagaggtacg cagaagcatc gtgccctgag gtcggacacc 120  
 aaactctcca tgtcaactcg ctgcaagggt aaaggagcat catgtcatag gacttcgtat 180  
 gactgctgca ccggttcttg caacagaggt aaatgtggct gatccggcgc ctgatcttcc 240  
 cccttctgtg ctctatcctt ttctgcctga gtcattccata cctgtgctcg ag 292

<210> 112  
 <211> 71  
 <212> PRT  
 <213> Conus consors

<400> 112  
 Met Lys Leu Thr Cys Met Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30

Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Gly  
 35 40 45

Lys Gly Ala Ser Cys His Arg Thr Ser Tyr Asp Cys Cys Thr Gly Ser  
 50 55 60

Cys Asn Arg Gly Lys Cys Gly  
 65 70

<210> 113  
 <211> 25  
 <212> PRT  
 <213> Conus consors

<220>  
 <221> PEPTIDE  
 <222> (1)..(25)  
 <223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 113  
 Cys Lys Gly Lys Gly Ala Ser Cys His Arg Thr Ser Xaa Asp Cys Cys  
 1 5 10 15

Thr Gly Ser Cys Asn Arg Gly Lys Cys  
 20 25

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<210> 114  
 <211> 299  
 <212> DNA  
 <213> Conus consors

<400> 114  
 ggatccatga aactgacgtg cgtggtgata gtcgccgtgc tgctcctgac ggctgtcaa 60  
 ctcatcacag ctgatgactc cagaggtacg cagaagcatt gtgccctgaa gtcggacacc 120  
 aaactctcca tgttaacttt gcgctgcgca tcttacggaa aaccttgtgg tatttacaac 180  
 gactgctgca atacatgcga tccagccaga aagacatgta cgtagctgat ccggcgtctg 240  
 atcttcccc ttctgtgctc tctcttttc tgctgagtc atesatacct gtgctcgag 299

<210> 115  
 <211> 72  
 <212> PRT  
 <213> Conus consors

<400> 115  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15  
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30  
 Ala Leu Lys Ser Asp Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Ala  
 35 40 45  
 Ser Tyr Gly Lys Pro Cys Gly Ile Tyr Asn Asp Cys Cys Asn Thr Cys  
 50 55 60  
 Asp Pro Ala Arg Lys Thr Cys Thr  
 65 70

<210> 116  
 <211> 26  
 <212> PRT  
 <213> Conus consors

<220>  
 <221> PEPTIDE  
 <222> (1)..(26)  
 <223> Xaa at residue 7 and 20 is Pro or Hyp; Xaa at residue 4 and 11 is  
 Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-pho  
 spho-Ty

<400> 116  
 Cys Ala Ser Xaa Gly Lys Xaa Cys Gly Ile Xaa Asn Asp Cys Cys Asn  
 1 5 10 15  
 Thr Cys Asp Xaa Ala Arg Lys Thr Cys Thr  
 20 25

<210> 117  
 <211> 434  
 <212> DNA  
 <213> Conus consors

<220>  
 <221> misc\_feature

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<222> (1)..(434)

<223> n may be any nucleotide

<400> 117

ggatccatga aactgacgtg tgtggtgac gtcgccgtgc tgctcctgac ggccctgtcaa 60

ctcatcacag ctgatgactc cagaggtacg cagaagcatc gtgccctgag gtcggacacc 120

aaactctcca tgtcgactcg ctgcaagggc acaggaaaac catgcagtag gggtgcgtat 180

aactgctgca ccggttcttg cagatcaggt aaatgtggct gatccagtgc ctgatcttcc 240

cccttctgtg ctctatcctt ttctgctga gtcctcctta cctgagagtg gtcatgaacc 300

actcatcacc tgctcctctg gaggtctcag aggagctaca ttgaaataaa agccgcattg 360

caatgnanaa aannnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnggaaaaaa 420

aaaaaaaaaa aaaa 434

<210> 118

<211> 71

<212> PRT

<213> Conus consors

<400> 118

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
20 25 30

Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Gly  
35 40 45

Thr Gly Lys Pro Cys Ser Arg Val Ala Tyr Asn Cys Cys Thr Gly Ser  
50 55 60

Cys Arg Ser Gly Lys Cys Gly  
65 70

<210> 119

<211> 25

<212> PRT

<213> Conus consors

<220>

<221> PEPTIDE

<222> (1)..(25)

<223> Xaa at residue 7 is Pro or Hyp; Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 119

Cys Lys Gly Thr Gly Lys Xaa Cys Ser Arg Val Ala Xaa Asn Cys Cys  
1 5 10 15

Thr Gly Ser Cys Arg Ser Gly Lys Cys  
20 25

<210> 120

<211> 393

<212> DNA

<213> Conus consors

<400> 120

00910082.072301

ggatccatga aactgacgtg catggtgatc gtcgccgtgc tgctcctgac ggcctgtcaa 60  
 ctcatcacag ctgatgactc cagaggtacg cagaagcatc gttccctgag gtcgaccacc 120  
 aaagtctcca agtcgactag ctgcatgaaa gccgggtctt attgccgctc tactacgaga 180  
 acctgctgcg gttattgcmc ttattttcggc aaatttttga ttgactttcc cagcaactga 240  
 tcttccccct actgtgctct atccttttct gcctctgcct gagtcctcct tacctgagag 300  
 tggatcatgaa ccaactcatca cctgctcccc tggaggcctc agaggagcta caatgaaata 360  
 aaagccgcat tgcaaaaaaa aaaaaaaaaa aaa 393

<210> 121

<211> 77

<212> PRT

<213> Conus consors

<400> 121

Met Lys Leu Thr Cys Met Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30

Ser Leu Arg Ser Thr Thr Lys Val Ser Lys Ser Thr Ser Cys Met Lys  
 35 40 45

Ala Gly Ser Tyr Cys Arg Ser Thr Thr Arg Thr Cys Cys Gly Tyr Cys  
 50 55 60

Ala Tyr Phe Gly Lys Phe Cys Ile Asp Phe Pro Ser Asn  
 65 70 75

<210> 122

<211> 35

<212> PRT

<213> Conus consors

<220>

<221> PEPTIDE

<222> (1)..(35)

<223> Xaa at residue 33 is Pro or Hyp; Xaa at residue 10, 21 and 24 is  
 Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phos  
 pho-Ty

<400> 122

Ser Thr Ser Cys Met Lys Ala Gly Ser Xaa Cys Arg Ser Thr Thr Arg  
 1 5 10 15

Thr Cys Cys Gly Xaa Cys Ala Xaa Phe Gly Lys Phe Cys Ile Asp Phe  
 20 25 30

Xaa Ser Asn  
 35

<210> 123

<211> 361

<212> DNA

<213> Conus dalli

<400> 123

acaaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgttctg

acggcctgtc aactcatcac agctgatgac tccagaagta cgcagaagca tcgtgctctg 120  
 aggtcgacca tcaaacactc catgttgact aggagctgca cgcctcccgg aggaccttgt 180  
 gggtattata atgactgctg cagtcacaa tgcaatataa gcagaaataa atgcgagtag 240  
 ctgatccggc atctgatctt ccccttctgt gctcgctcta acctgagagt ggtcatgaac 300  
 catcatcacc tactcctctg gaggcttcag aggagctaca tggaaataaa agccgcattg 360  
 c 361

<210> 124  
 <211> 73  
 <212> PRT  
 <213> Conus dalli

<400> 124  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15  
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Ser Thr Gln Lys His Arg  
 20 25 30  
 Ala Leu Arg Ser Thr Ile Lys His Ser Met Leu Thr Arg Ser Cys Thr  
 35 40 45  
 Pro Pro Gly Gly Pro Cys Gly Tyr Tyr Asn Asp Cys Cys Ser His Gln  
 50 55 60  
 Cys Asn Ile Ser Arg Asn Lys Cys Glu  
 65 70

<210> 125  
 <211> 28  
 <212> PRT  
 <213> Conus dalli

<220>  
 <221> PEPTIDE  
 <222> (1)..(28)  
 <223> Xaa at residue 28 is Glu or gamma-carboxy Glu; Xaa at residue 4,  
 5 and 8 is Pro or Hyp; Xaa at residue 11 and 12 is Tyr, 125I-Tyr,  
 mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 125  
 Ser Cys Thr Xaa Xaa Gly Gly Xaa Cys Gly Xaa Xaa Asn Asp Cys Cys  
 1 5 10 15  
 Ser His Gln Cys Asn Ile Ser Arg Asn Lys Cys Xaa  
 20 25

<210> 126  
 <211> 350  
 <212> DNA  
 <213> Conus distans

<400> 126  
 accaaaacca tcâtcaaaat gaaactgacg tgcgtgttga tcatcgccgt gctgttcttg 60  
 acggcctgtc aactcactag aggaaagctg gagcgtcctg ttctgagggtc gagcgaccaa 120  
 acctccgggt caacgaagag atgcgaagat cctgggtgaac cttgcggaag tgatcattcc 180  
 tgctgcggcg gtagttgcaa ccacaacgtc tgcgcctgaa gctgggtctgg catctgacca 240

0910082 072301

ttcccccttct gtactctatc tctattgcct gagtcatctt tacctgtgag tggatcatgaa 300

tctctcaata ccttctcccc tggaggcttc agaagaacta gattgaaata 350

<210> 127

<211> 66

<212> PRT

<213> Conus distans

<400> 127

Met Lys Leu Thr Cys Val Leu Ile Ile Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Cys Gln Leu Thr Arg Gly Lys Leu Glu Arg Pro Val Leu Arg Ser Ser  
20 25 30

Asp Gln Thr Ser Gly Ser Thr Lys Arg Cys Glu Asp Pro Gly Glu Pro  
35 40 45

Cys Gly Ser Asp His Ser Cys Cys Gly Gly Ser Cys Asn His Asn Val  
50 55 60

Cys Ala  
65

<210> 128

<211> 25

<212> PRT

<213> Conus distans

<220>

<221> PEPTIDE

<222> (1)..(25)

<223> Xaa at residue 2 and 6 is Glu or gamma-carboxy Glu; Xaa at residue 4 and 7 is Pro or Hy

<400> 128

Cys Xaa Asp Xaa Gly Xaa Xaa Cys Gly Ser Asp His Ser Cys Cys Gly  
1 5 10 15

Gly Ser Cys Asn His Asn Val Cys Ala  
20 25

<210> 129

<211> 309

<212> DNA

<213> Conus ermineus

<400> 129

atgaaactga cgtgtgtggt gatcgctgcc gtgctgctcc tgacggcctg tcaactcatc 60

acagctgacg actccagacg tacgcagaag catcgtgccc tgaggctgac caccaaacgc 120

gccacgtcga atcgcccctg caagccgaaa ggacgaaaat gttttccgca tcagaaggac 180

tgctgcaata aaacgtgcac cagatcaaaa tgtccctgat cttccccctt ctgtgctgta 240

tccttttctg cctgagtcct cttacctga gagtggtcag taaccactca tcaccatctc 300

ctctggagg 309

<210> 130

<211> 72

<212> PRT

00910082 072301

<213> Conus ermineus

<400> 130

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Arg Thr Gln Lys His Arg  
20 25 30

Ala Leu Arg Ser Thr Thr Lys Arg Ala Thr Ser Asn Arg Pro Cys Lys  
35 40 45

Pro Lys Gly Arg Lys Cys Phe Pro His Gln Lys Asp Cys Cys Asn Lys  
50 55 60

Thr Cys Thr Arg Ser Lys Cys Pro  
65 70

<210> 131

<211> 27

<212> PRT

<213> Conus ermineus

<220>

<221> PEPTIDE

<222> (1)..(27)

<223> Xaa at residue 1, 4, 11 and 27 is Pro or Hyp

<400> 131

Xaa Xaa Lys Xaa Lys Gly Arg Lys Cys Phe Xaa His Gln Lys Asp Cys  
1 5 10 15

Cys Asn Lys Thr Cys Thr Arg Ser Lys Cys Xaa  
20 25

<210> 132

<211> 308

<212> DNA

<213> Conus ermineus

<400> 132

aactcatcac agctgatgac tccagaggta cgcagaacga tcgtgccctg aggtcgacca 60

ccaaactctc catgctgact cgggcctgct ggtcttcgag aacaccttgt ggtactgata 120

gtttatgctg cggtggatgc aatgtatcca aaagtaaag taactagctg attcggcgctc 180

tgaacttccc cttctgtgct tctatccttt tctgcccagag tctccatac ctgagaatgg 240

tcatgaacca ctcatcacct actcctctgg agacctcaga agagctacac tgaataaaaa 300

gcgcttgc 308

<210> 133

<211> 54

<212> PRT

<213> Conus ermineus

<400> 133

Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Asn Asp Arg Ala Leu  
1 5 10 15

Arg Ser Thr Thr Lys Leu Ser Met Leu Thr Arg Ala Cys Trp Ser Ser  
20 25 30

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Gly Thr Pro Cys Gly Thr Asp Ser Leu Cys Cys Gly Gly Cys Asn Val  
 35 40 45

Ser Lys Ser Lys Cys Asn  
 50

<210> 134

<211> 27

<212> PRT

<213> Conus ermineus

<220>

<221> PEPTIDE

<222> (1)..(27)

<223> Xaa at 8 residue is Pro or Hyp; Xaa at residue 3 is Trp or Bromo  
 Tr

<400> 134

Ala Cys Xaa Ser Ser Gly Thr Xaa Cys Gly Thr Asp Ser Leu Cys Cys  
 1 5 10 15

Gly Gly Cys Asn Val Ser Lys Ser Lys Cys Asn  
 20 25

<210> 135

<211> 385

<212> DNA

<213> Conus geographus

<400> 135

ggatccatga aactgacgtg cgtggtgatc gtcgccgtgc tgctcctgac ggctgtgcaa 60

ctcatcacag ctgatgactc cagaggtacg cagaagcadc gtgccctggg gtcgaccacc 120

gaactctcct tgtcgactcg ctgcaagtca cccggatctt catgttcacc gactagttat 180

aattgctgca ggtcttgcaa tccatacgcc aaaagatggt acggctaadc cagcgccctga 240

tcttccccct tctgtgctct atcccttctt gtctgagtc tcttacctg agagtggatca 300

tgaaccactc ctcacctact tctctggagg cttcggagga gctacattga aataaaagcc 360

gcattgtaaa aaaaaaaaaa aaaaa 385

<210> 136

<211> 73

<212> PRT

<213> Conus geographus

<400> 136

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30

Ala Leu Gly Ser Thr Thr Glu Leu Ser Leu Ser Thr Arg Cys Lys Ser  
 35 40 45

Pro Gly Ser Ser Cys Ser Pro Thr Ser Tyr Asn Cys Cys Arg Ser Cys  
 50 55 60

Asn Pro Tyr Ala Lys Arg Cys Tyr Gly  
 65 70

09910082.0230

<210> 137  
 <211> 27  
 <212> PRT  
 <213> Conus geographus

<220>  
 <221> PEPTIDE  
 <222> (1)..(27)  
 <223> Xaa at residue 4, 10 and 21 is Pro or Hyp; Xaa at residue 13, 22  
 and 27 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr  
 or O-phospho-Ty

<400> 137  
 Cys Lys Ser Xaa Gly Ser Ser Cys Ser Xaa Thr Ser Xaa Asn Cys Cys  
 1 5 10 15

Arg Ser Cys Asn Xaa Xaa Ala Lys Arg Cys Xaa  
 20 25

<210> 138  
 <211> 396  
 <212> DNA  
 <213> Conus geographus

<400> 138  
 ggatccatga aactgacgtg tgtggtgatc gtcgccgtgc tgctcctgac ggctgtgtcaa 60  
 ctcatcacag ctgatgactc cagaggtacg cagaagcattc gtgccctgag gtcgtccacc 120  
 aaactcacct tgtcgactcg ctgcaaatca cccggaactc catgttcaag gggtatgcgt 180  
 gattgctgca cgccttgctt gttatacagc aacaaatgta ggcgctacta acccagcgcc 240  
 tgatcttccc ccttctgtgc tctattcctt tctgcttgag tctccttac ctgaaagtgg 300  
 tcatgaacca ctcatcacct acttctctgg aggttcaga agagctacat tgaaataaaa 360  
 gccgcattgc aatgacaaaa aaaaaaaaaa aaaaaa 396

<210> 139  
 <211> 74  
 <212> PRT  
 <213> Conus geographus

<400> 139  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30

Ala Leu Arg Ser Ser Thr Lys Leu Thr Leu Ser Thr Arg Cys Lys Ser  
 35 40 45

Pro Gly Thr Pro Cys Ser Arg Gly Met Arg Asp Cys Cys Thr Pro Cys  
 50 55 60

Leu Leu Tyr Ser Asn Lys Cys Arg Arg Tyr  
 65 70

<210> 140  
 <211> 29  
 <212> PRT  
 <213> Conus geographus

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<220>  
 <221> PEPTIDE  
 <222> (1)..(29)  
 <223> Xaa at residue 4, 7 and 18 is Pro or Hyp; Xaa at residue 22 and 29 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 140  
 Cys Lys Ser Xaa Gly Thr Xaa Cys Ser Arg Gly Met Arg Asp Cys Cys  
 1 5 10 15

Thr Xaa Cys Leu Leu Xaa Ser Asn Lys Cys Arg Arg Xaa  
 20 25

<210> 141

<211> 407

<212> DNA

<213> Conus geographus

<400> 141  
 ggaattccgt ttctgcgctg cttcctttgg catcaccaaa accatcatca aaatgaaact 60  
 gacgtgtgtg gtgatcgctg ccgtgctgct cctgacggcc tgtcaactca tcacagctga 120  
 tgactccaga ggtacgcaga agcatcgctg cctggggctg accaccgaac tctccttgctc 180  
 gactcgctgc aagtcacccg gatcttcatg ttcaccgact agttataatt gctgcaggctc 240  
 ttgcaatcca tacaccaaaa gatgttacgg ctaatccagc gcctgatctt ccctgctctg 300  
 agtcctcctt acctgagagt ggtcatgaac cactcatcac ctacttctct aggcgggttcg 360  
 gaggagctac attgaaataa aagccgcatt gcaaaaaaaaa aaaaaaaa 407

<210> 142

<211> 73

<212> PRT

<213> Conus geographus

<400> 142  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30

Ala Leu Gly Ser Thr Thr Glu Leu Ser Leu Ser Thr Arg Cys Lys Ser  
 35 40 45

Pro Gly Ser Ser Cys Ser Pro Thr Ser Tyr Asn Cys Cys Arg Ser Cys  
 50 55 60

Asn Pro Tyr Thr Lys Arg Cys Tyr Gly  
 65 70

<210> 143

<211> 27

<212> PRT

<213> Conus geographus

<220>

<221> PEPTIDE

<222> (1)..(27)

<223> Xaa at residue 4, 10 and 21 is Pro or Hyp; Xaa at residue 13, 22 and 27 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr

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or O-phospho-Ty

<400> 143

Cys Lys Ser Xaa Gly Ser Ser Cys Ser Xaa Thr Ser Xaa Asn Cys Cys  
1 5 10 15

Arg Ser Cys Asn Xaa Xaa Thr Lys Arg Cys Xaa  
20 25

<210> 144

<211> 28

<212> PRT

<213> Conus geographus

<220>

<221> PEPTIDE

<222> (1)..(28)

<223> Xaa at residue 4, 10 and 21 is Pro or Hyp; Xaa at residue 13, 22  
and 27 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr  
or O-phospho-Ty

<400> 144

Cys Lys Ser Xaa Gly Ser Ser Cys Ser Xaa Thr Ser Xaa Asn Cys Cys  
1 5 10 15

Arg Ser Cys Asn Xaa Xaa Thr Lys Arg Cys Xaa Gly  
20 25

<210> 145

<211> 26

<212> PRT

<213> Conus geographus

<220>

<221> PEPTIDE

<222> (1)..(26)

<223> Xaa at residue 4, 10 and 21 is Pro or Hyp; Xaa at residue 13 and  
22 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or  
O-phospho-Ty

<400> 145

Cys Lys Ser Xaa Gly Ser Ser Cys Ser Xaa Thr Ser Xaa Asn Cys Cys  
1 5 10 15

Arg Ser Cys Asn Xaa Xaa Thr Lys Arg Cys  
20 25

<210> 146

<211> 314

<212> DNA

<213> Conus geographus

<400> 146

catcacagct gatgactcca gaggtacgca gaagcatcgt gccctgaggt cgtccaccaa 60  
actcaccttg tcgactcgct gcaaatacacc cggaactcca tgttcaaggg gtatgcgtga 120  
ttgctgcacg tcttgcttgt tatacagcaa caaatgtagg cgctactaac ccagcgctg 180  
atcttcccc ttctgtgctc tattcctttc tgctgagtc ctccttacct gaaagtggtc 240  
atgaaccact catcacctac ttctctggag gcttcagaag agctacattg aaataaaagc 300  
cgattgcaa tgac 314

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<210> 147  
 <211> 55  
 <212> PRT  
 <213> Conus geographus

<400> 147  
 Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg Ala Leu Arg  
 1 5 10 15  
 Ser Ser Thr Lys Leu Thr Leu Ser Thr Arg Cys Lys Ser Pro Gly Thr  
 20 25 30  
 Pro Cys Ser Arg Gly Met Arg Asp Cys Cys Thr Ser Cys Leu Leu Tyr  
 35 40 45  
 Ser Asn Lys Cys Arg Arg Tyr  
 50 55

<210> 148  
 <211> 29  
 <212> PRT  
 <213> Conus geographus  
 <220>  
 <221> PEPTIDE  
 <222> (1)..(29)  
 <223> Xaa at residue 4 and 7 is Pro or Hyp; Xaa at residue 22 and 29 is  
 Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-pho  
 spho-Ty

<400> 148  
 Cys Lys Ser Xaa Gly Thr Xaa Cys Ser Arg Gly Met Arg Asp Cys Cys  
 1 5 10 15  
 Thr Ser Cys Leu Leu Xaa Ser Asn Lys Cys Arg Arg Xaa  
 20 25

<210> 149  
 <211> 29  
 <212> PRT  
 <213> Conus geographus

<220>  
 <221> PEPTIDE  
 <222> (1)..(29)  
 <223> Xaa at residue 4 and 7 is Pro or Hyp; Xaa at residue 22 and 29 is  
 Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-pho  
 spho-Ty

<400> 149  
 Cys Lys Ser Xaa Gly Thr Xaa Cys Ser Arg Gly Met Arg Asp Cys Cys  
 1 5 10 15  
 Thr Ser Cys Leu Ser Xaa Ser Asn Lys Cys Arg Arg Xaa  
 20 25

<210> 150  
 <211> 380  
 <212> DNA  
 <213> Conus laterculatus

<400> 150  
 accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60  
 acggcctgtc aactcatcac cgctgatgac tccagaggta cgcagaagca tcgtgcctg 120

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aggtcgacca ccaatctctc catgctgact cggaagtgct ggccttccgg aagctattgt 180  
 cgtgcgaata gtaaagtctg cagtggatgc gatcggaaca gaaataaatg ttactagctg 240  
 attcggcgtc tgaacttcct ctttctgtgc tctatccttt tctgcccagag tcctccatac 300  
 ctgagagtgg tcatgaacca ctcaactcct actcctctgg aggcctcaga agagctacat 360  
 tgaaataaaaa gccgcattgc 380

<210> 151  
 <211> 72  
 <212> PRT  
 <213> Conus laterculatus

<400> 151

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30

Ala Leu Arg Ser Thr Thr Asn Leu Ser Met Leu Thr Arg Lys Cys Trp  
 35 40 45

Pro Ser Gly Ser Tyr Cys Arg Ala Asn Ser Lys Cys Cys Ser Gly Cys  
 50 55 60

Asp Arg Asn Arg Asn Lys Cys Tyr  
 65 70

<210> 152  
 <211> 27  
 <212> PRT  
 <213> Conus laterculatus

<220>

<221> PEPTIDE

<222> (1)..(27)

<223> Xaa at residue 4 is Pro or Hyp; Xaa at residue 3 is Trp or Bromo  
 Trp; Xaa at residue 8 and 27 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-  
 iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 152

Lys Cys Xaa Xaa Ser Gly Ser Xaa Cys Arg Ala Asn Ser Lys Cys Cys  
 1 5 10 15

Ser Gly Cys Asp Arg Asn Arg Asn Lys Cys Xaa  
 20 25

<210> 153  
 <211> 367  
 <212> DNA  
 <213> Conus laterculatus

<400> 153

acaaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60

acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccttg 120

aggtcgacca ccaaactctc catatcgact cgctgccttc ctcccggatc atattgtaag 180

gcgacaacgg aagtctgctg ctcttcttgc cttcaattcg ctcagatatg ttcgggttga 240

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tcttccctct tctgtgctct atccttttct gcctgagtc tccatacctg agaatggta 300  
 tgaaccactc aacatctact cctctggagg cctcagaaga gctatattga aataaaagcc 360  
 gcattgc 367

<210> 154  
 <211> 73  
 <212> PRT  
 <213> Conus laterculatus

<400> 154  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30

Ala Leu Arg Ser Thr Thr Lys Leu Ser Ile Ser Thr Arg Cys Leu Pro  
 35 40 45

Pro Gly Ser Tyr Cys Lys Ala Thr Thr Glu Val Cys Cys Ser Ser Cys  
 50 55 60

Leu Gln Phe Ala Gln Ile Cys Ser Gly  
 65 70

<210> 155  
 <211> 27  
 <212> PRT  
 <213> Conus laterculatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(27)  
 <223> Xaa at residue 13 is Glu or gamma-carboxy Glu; Xaa at residue 3 and 4 is Pro or Hyp; Xaa at residue 7 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 155  
 Cys Leu Xaa Xaa Gly Ser Xaa Cys Lys Ala Thr Thr Xaa Val Cys Cys  
 1 5 10 15

Ser Ser Cys Leu Gln Phe Ala Gln Ile Cys Ser  
 20 25

<210> 156  
 <211> 373  
 <212> DNA  
 <213> Conus laterculatus

<400> 156  
 accaaaacca tcatcaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60  
 acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccctg 120  
 aggtcgacca ccaatctctc catgtcgact cgctgcaagt ctcccgaatc atcatgtagc 180  
 gtgtctatgc gtaactgctg cacttcttgc aattcacgca ccaagaaatg tacgcgacgt 240  
 ggctgaactt ccccttctg tgctctatcc ttttctgccc gagtcctcca tacctgagag 300  
 tggatcatgaa ccactcaaca tctactcctc tggaggcctc agaagagcta tattgaaata 360  
 aaagccgcac tgc 373

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Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
20 25 30

Ala Leu Arg Ser Thr Thr Lys Leu Ser Met Leu Thr Arg Thr Cys Trp  
35 40 45

Pro Ser Gly Thr Ala Cys Gly Ile Asp Ser Asn Cys Cys Ser Gly Cys  
50 55 60

Asn Val Ser Arg Ser Lys Cys Asn  
65 70

<210> 161

<211> 27

<212> PRT

<213> *Conus laterculatus*

<220>

<221> PEPTIDE

<222> (1)..(27)

<223> Xaa at residue 4 is Pro or Hyp; Xaa at residue 3 is Trp or Bromo  
Tr

<400> 161

Thr Cys Xaa Xaa Ser Gly Thr Ala Cys Gly Ile Asp Ser Asn Cys Cys  
1 5 10 15

Ser Gly Cys Asn Val Ser Arg Ser Lys Cys Asn  
20 25

<210> 162

<211> 363

<212> DNA

<213> *Conus laterculatus*

<400> 162

accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60

acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccctg 120

aggtcgacca ccaatctctc catgctgact cggaagtgtt ggccttccgg aagctattgt 180

cgtgcgaata gtaaattgctg cagtggatgc gatcggaaca gaagtaaattg taactagctg 240

attcggcgctc taaacttcct cttctgcct gagtcctcca tacctgagag tggatcatgaa 300

ccactcatca cctactcctc tggaggcctc aaaggagcta cattgaaata aaagccgcat 360

tgc 363

<210> 163

<211> 72

<212> PRT

<213> *Conus laterculatus*

<400> 163

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
20 25 30

Ala Leu Arg Ser Thr Thr Asn Leu Ser Met Leu Thr Arg Lys Cys Trp  
35 40 45

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Pro Ser Gly Ser Tyr Cys Arg Ala Asn Ser Lys Cys Cys Ser Gly Cys  
 50 55 60

Asp Arg Asn Arg Ser Lys Cys Asn  
 65 70

<210> 164

<211> 27

<212> PRT

<213> Conus laterculatus

<220>

<221> PEPTIDE

<222> (1)..(27)

<223> Xaa at residue4 is Pro or Hyp; Xaa at residue 3 is Trp or Bromo  
 Trp; Xaa at residue 8 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Ty  
 r, O-sulpho-Tyr or O-phospho-Ty

<400> 164

Lys Cys Xaa Xaa Ser Gly Ser Xaa Cys Arg Ala Asn Ser Lys Cys Cys  
 1 5 10 15

Ser Gly Cys Asp Arg Asn Arg Ser Lys Cys Asn  
 20 25

<210> 165

<211> 391

<212> DNA

<213> Conus leopardus

<220>

<221> misc\_feature

<222> (1)..(391)

<223> n may be any nucleotide

<400> 165

atgaaactga cgtgtgtggt gatcgtagct gtgctgttcc tgacggcctg tcaactcact 60  
 acagctgaca tctccagagg tacgcggaag cgctgtgctc tgaggctcgac caccaaactc 120  
 tccaggtcgc tctttgagtg cgcgcttcc ggtggacgtt gtgggttttt aaagtccctgc 180  
 tgcaaggat attgcgatgg ggaaagcact tcatgtgtga gtggcccata cagcatctga 240  
 tcttcccgcc ttcagtgtc tatccttttc tgcttgagtc ctccatacct ctgagcggtc 300  
 atgaaccact caacacctac tctctggag gcttcaggga actatattaa aataaagccg 360  
 cattgcaacg aaanaaaaaa aaaaaaaaaa a 391

<210> 166

<211> 79

<212> PRT

<213> Conus leopardus

<400> 166

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Thr Thr Ala Asp Ile Ser Arg Gly Thr Arg Lys Arg Arg  
 20 25 30

Ala Leu Arg Ser Thr Thr Lys Leu Ser Arg Ser Leu Phe Glu Cys Ala  
 35 40 45

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Pro Ser Gly Gly Arg Cys Gly Phe Leu Lys Ser Cys Cys Glu Gly Tyr  
50 55 60

Cys Asp Gly Glu Ser Thr Ser Cys Val Ser Gly Pro Tyr Ser Ile  
65 70 75

<210> 167

<211> 37

<212> PRT

<213> Conus leopardus

<220>

<221> PEPTIDE

<222> (1)..(37)

<223> Xaa at residue 4, 20 and 26 is Glu or gamma-carboxy Glu; Xaa at r  
esidue 7 and 34 is Pro or Hyp; Xaa at residue 22 and 35 is Tyr,  
125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-T  
y

<400> 167

Ser Leu Phe Xaa Cys Ala Xaa Ser Gly Gly Arg Cys Gly Phe Leu Lys  
1 5 10 15

Ser Cys Cys Xaa Gly Xaa Cys Asp Gly Xaa Ser Thr Ser Cys Val Ser  
20 25 30

Gly Xaa Xaa Ser Ile  
35

<210> 168

<211> 365

<212> DNA

<213> Conus leopardus

<400> 168

atgaaactga cgtgtgtggt gatcgctcgct gtgctgttcc tgacggcctg tcaactcact 60

acagctgaca tctccagagg tacgtggaag catcggtggtg tggggtcgac caccggactc 120

tccccgtggc ccttggactg cacggctccc agtcaacctt gtggttatatt tcttaggtgc 180

tgtggacatt gcgatgtacg cagggtatgt acgagtggct gatccggcgt ctgatcttctc 240

cgcccttctgt gctgtatcct tttctgcctg agtcctccat acccgtgagt ggtcatgaac 300

cactcaacac ctactcctct ggaggcttca gaggaactat attaaaataa agccgcattg 360

caatg 365

<210> 169

<211> 73

<212> PRT

<213> Conus leopardus

<400> 169

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Cys Gln Leu Thr Thr Ala Asp Ile Ser Arg Gly Thr Trp Lys His Arg  
20 25 30

Gly Val Gly Ser Thr Thr Gly Leu Ser Pro Trp Pro Leu Asp Cys Thr  
35 40 45

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Ala Pro Ser Gln Pro Cys Gly Tyr Phe Pro Arg Cys Cys Gly His Cys  
50 55 60

Asp Val Arg Arg Val Cys Thr Ser Gly  
65 70

<210> 170

<211> 30

<212> PRT

<213> Conus leopardus

<220>

<221> PEPTIDE

<222> (1)..(30)

<223> Xaa at residue 2, 8, 11 and 16 is Pro or Hyp; Xaa at residue 1 is  
Trp or Bromo Trp; Xaa at residue 14 is Tyr, 125I-Tyr, mono-iodo-  
Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 170

Xaa Xaa Leu Asp Cys Thr Ala Xaa Ser Gln Xaa Cys Gly Xaa Phe Xaa  
1 5 10 15

Arg Cys Cys Gly His Cys Asp Val Arg Arg Val Cys Thr Ser  
20 25 30

<210> 171

<211> 381

<212> DNA

<213> Conus leopardus

<400> 171

atgaaactga cgtgtgtggt gatcgtcgct gtgctgttcc tgacggcctg tcaactcact 60  
acagctgaca tctccagagg tacgcggaag catcgtgctc tgaggctcgac caccaaactc 120  
tccaggctgc cctctaggtg catgtctccc ggtggaattt gtggtgattt tgggtgactgc 180  
tgcgaaattt gcaatgtgta cggtatatgt gtgagtact taccggcat ctgatcttc 240  
cgcttctgt gctctatcct tttctgcctg agtctccat acccctgagt ggtcatggac 300  
caactcaacac ctactcctct ggaggcttca gaggaactac attaaaataa agccgcattg 360  
caaaaaaaaa aaaaaaaaaa a 381

<210> 172

<211> 77

<212> PRT

<213> Conus leopardus

<400> 172

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Cys Gln Leu Thr Thr Ala Asp Ile Ser Arg Gly Thr Arg Lys His Arg  
20 25 30

Ala Leu Arg Ser Thr Thr Lys Leu Ser Arg Ser Pro Ser Arg Cys Met  
35 40 45

Ser Pro Gly Gly Ile Cys Gly Asp Phe Gly Asp Cys Cys Glu Ile Cys  
50 55 60

Asn Val Tyr Gly Ile Cys Val Ser Asp Leu Pro Gly Ile  
65 70 75

<210> 173  
 <211> 31  
 <212> PRT  
 <213> Conus leopardus

<220>  
 <221> PEPTIDE  
 <222> (1)..(31)  
 <223> Xaa at residue 16 is Glu or gamma-carboxy Glu; Xaa at residue 4 and 29 is Pro or Hyp; Xaa at residue 21 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 173  
 Cys Met Ser Xaa Gly Gly Ile Cys Gly Asp Phe Gly Asp Cys Cys Xaa  
 1 5 10 15

Ile Cys Asn Val Xaa Gly Ile Cys Val Ser Asp Leu Xaa Gly Ile  
 20 25 30

<210> 174  
 <211> 404  
 <212> DNA  
 <213> Conus leopardus

<400> 174  
 atgaaactga cgtgtgtggt gatcgtcgct gtgctgttcc tgacggcctg tcaactcact 60  
 acagctgatg attccagagg tacacggaag catcgtgctc tgagggtcaac caccaaactc 120  
 tccaggtggc ccaggtactg cgcgcctccc ggtggagctt gtgggttttt tgatcactgc 180  
 tgcggatatt gcgaaacgtt ttacaatacg tgtagatgag ttggctgata cggcgcttga 240  
 tctttccgcc ttctgttgct ctatcttttt ctgcctgagt cctcccatac cccgttgagt 300  
 ggtccatgaa ccaactccaac acctactccc tcttggaag cttccaaagg aaacgacatt 360  
 taaaataaat tccccattgc aattggaaaa aaaaaaaaaa aaaa 404

<210> 175  
 <211> 72  
 <212> PRT  
 <213> Conus leopardus

<400> 175  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Thr Thr Ala Asp Asp Ser Arg Gly Thr Arg Lys His Arg  
 20 25 30

Ala Leu Arg Ser Thr Thr Lys Leu Ser Arg Trp Pro Arg Tyr Cys Ala  
 35 40 45

Pro Pro Gly Gly Ala Cys Gly Phe Phe Asp His Cys Cys Gly Tyr Cys  
 50 55 60

Glu Thr Phe Tyr Asn Thr Cys Arg  
 65 70

<210> 176  
 <211> 27  
 <212> PRT  
 <213> Conus leopardus

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<220>  
 <221> PEPTIDE  
 <222> (1)..(27)  
 <223> Xaa at residue 20 is Glu or gamma-carboxy Glu; Xaa at residue 4 and 5 is Pro or Hyp; Xaa at residue 1, 18 and 23 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 176  
 Xaa Cys Ala Xaa Xaa Gly Gly Ala Cys Gly Phe Phe Asp His Cys Cys  
 1 5 10 15

Gly Xaa Cys Xaa Thr Phe Xaa Asn Thr Cys Arg  
 20 25

<210> 177  
~~<211> 292~~  
 <212> DNA  
 <213> Conus lynceus

<400> 177  
 atgaaactga cgtgtgtggt gatcgctcgcc gtgctgctcc tgacggcctg tcaactcatc 60  
 acagctgatg actccagacg tacacagaag catcggtgccc tgagggtcgac caccaatctc 120  
 tccatgtcga ctgctgcaa gtctcccga tcaccatgta gtgtgacatc gtataactgc 180  
 tgcacttttt gctcttcata cactaagaaa tgtcgggcct ctttatgaac cactcatcac 240  
 ctactcctct ggaggcctca gaagagctac actgaaataa aagccgcatt gg 292

<210> 178  
 <211> 75  
 <212> PRT  
 <213> Conus lynceus

<400> 178  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Arg Thr Gln Lys His Arg  
 20 25 30

Ala Leu Arg Ser Thr Thr Asn Leu Ser Met Ser Thr Arg Cys Lys Ser  
 35 40 45

Pro Gly Ser Pro Cys Ser Val Thr Ser Tyr Asn Cys Cys Thr Phe Cys  
 50 55 60

Ser Ser Tyr Thr Lys Lys Cys Arg Ala Ser Leu  
 65 70 75

<210> 179  
 <211> 30  
 <212> PRT  
 <213> Conus lynceus

<220>  
 <221> PEPTIDE  
 <222> (1)..(30)  
 <223> Xaa at residue 4 and 7 is Pro or Hyp; Xaa at residue 13 and 22 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 179

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Cys Lys Ser Xaa Gly Ser Xaa Cys Ser Val Thr Ser Xaa Asn Cys Cys  
1 5 10 15

Thr Phe Cys Ser Ser Xaa Thr Lys Lys Cys Arg Ala Ser Leu  
20 25 30

<210> 180  
<211> 355  
<212> DNA  
<213> Conus lynceus

<400> 180  
atgaaactga cgtgtgtggt gatcgctgcc gtgctgctcg tgacggcctg tcaactcatc 60  
acagctgatg actccagagg tacgcagaag catcgctgcc tgaggctcgac caccaaacta 120

tccatgtata-ctcgctgccc aggtccagga gcaatttgtc ctaatagggt atgctgctggt 180  
tattgcagta aaagaacaca tctatgtcat tcgcgaactg gctgatcttc ccccttctgt 240  
gctctatcct ttttctgcct gagtcctcca tacctgagaa tggatcatgaa ccaactcatca 300  
cctactcctc ttggagacct cagaggagct aactgaaat aaaagccgca ttggc 355

<210> 181  
<211> 74  
<212> PRT  
<213> Conus lynceus

<400> 181  
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
20 25 30

Ala Leu Arg Ser Thr Thr Lys Leu Ser Met Tyr Thr Arg Cys Ala Gly  
35 40 45

Pro Gly Ala Ile Cys Pro Asn Arg Val Cys Cys Gly Tyr Cys Ser Lys  
50 55 60

Arg Thr His Leu Cys His Ser Arg Thr Gly  
65 70

<210> 182  
<211> 28  
<212> PRT  
<213> Conus lynceus

<220>  
<221> PEPTIDE  
<222> (1)..(28)  
<223> Xaa at residue 4 and 9 is Pro or Hyp; Xaa at residue 16 is Tyr, 1  
25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 182  
Cys Ala Gly Xaa Gly Ala Ile Cys Xaa Asn Arg Val Cys Cys Gly Xaa  
1 5 10 15

Cys Ser Lys Arg Thr His Leu Cys His Ser Arg Thr  
20 25

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<210> 183  
 <211> 361  
 <212> DNA  
 <213> Conus lynceus

<400> 183  
 atgaaactga cgtgtgtggt gatcgtcgcc gtgctgctgc tagcggcctg tcaactacta 60  
 cacgctgatg actccagagg tacgcagaag actgctgccc gaggtcgacc accaaaactc 120  
 tccatgctga ctcgggcctg ctgggtcttcc ggaacacctt gtggtactga tagtttatgc 180  
 tgcggtggat gcaatgtatc caaaagtaaa tgtaactagc tgattcggcg tctgaacttc 240  
 ccccttctgt gctctatcct tttctgccc agtcctccat acctgagaat ggtcatgaac 300  
 cactcatcac ctactcctct ggagacctca gaagagctac actgaaataa aagcgcattg 360  
 c 361

<210> 184  
 <211> 72  
 <212> PRT  
 <213> Conus lynceus

<400> 184  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Ala Ala  
 1 5 10 15  
 Cys Gln Leu Leu His Ala Asp Asp Ser Arg Gly Thr Gln Lys Thr Ala  
 20 25 30  
 Ala Arg Gly Arg Pro Pro Lys Leu Ser Met Leu Thr Arg Ala Cys Trp  
 35 40 45  
 Ser Ser Gly Thr Pro Cys Gly Thr Asp Ser Leu Cys Cys Gly Gly Cys  
 50 55 60  
 Asn Val Ser Lys Ser Lys Cys Asn  
 65 70

<210> 185  
 <211> 27  
 <212> PRT  
 <213> Conus lynceus

<220>  
 <221> PEPTIDE  
 <222> (1)..(27)  
 <223> Xaa at residue 8 is Pro or Hyp; Xaa at residue 3 is Trp or Bromo  
 Tr

<400> 185  
 Ala Cys Xaa Ser Ser Gly Thr Xaa Cys Gly Thr Asp Ser Leu Cys Cys  
 1 5 10 15  
 Gly Gly Cys Asn Val Ser Lys Ser Lys Cys Asn  
 20 25

<210> 186  
 <211> 364  
 <212> DNA  
 <213> Conus lynceus

<400> 186

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atgaaactga cgtgtgtggt gatcgtcgcc gagctactcc taacggcctg tcaactcatc 60  
 acagctgatg actccagagg tacgcagaag catcgtgccc tgaggctcgac caccaatctc 120  
 tccatgctga ctcggaagtg ctgggtctccc ggaacctatt gtcgtgcgca tagtaaatgc 180  
 tgccgtggat gcgatcagaa cagaaataaa tgttactagc tgattcggcg tctgaacttc 240  
 ctcttctgt gctctatcct ttttctgcct gagtcctcca tacctgagaa tggatcatgaa 300  
 ccaactcatca cctactcttc tggaggcctc agaggagcct aactgaaat aaaagccgca 360  
 ttgg 364

&lt;210&gt; 187

&lt;211&gt; 72

&lt;212&gt; PRT

&lt;213&gt; Conus lynceus

&lt;400&gt; 187

Met Lys Leu Thr Cys Val Val Ile Val Ala Glu Leu Leu Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30

Ala Leu Arg Ser Thr Thr Asn Leu Ser Met Leu Thr Arg Lys Cys Trp  
 35 40 45

Ser Pro Gly Thr Tyr Cys Arg Ala His Ser Lys Cys Cys Arg Gly Cys  
 50 55 60

Asp Gln Asn Arg Asn Lys Cys Tyr  
 65 70

&lt;210&gt; 188

&lt;211&gt; 27

&lt;212&gt; PRT

&lt;213&gt; Conus lynceus

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(27)

<223> Xaa at residue 5 is Pro or Hyp; Xaa at residue 3 is Trp or Bromo  
 Trp; Xaa at residue 8 and 27 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-  
 iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

&lt;400&gt; 188

Lys Cys Xaa Ser Xaa Gly Thr Xaa Cys Arg Ala His Ser Lys Cys Cys  
 1 5 10 15

Arg Gly Cys Asp Gln Asn Arg Asn Lys Cys Xaa  
 20 25

&lt;210&gt; 189

&lt;211&gt; 318

&lt;212&gt; DNA

&lt;213&gt; Conus magus

&lt;400&gt; 189

acaaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60

acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccctg 120

aggtcggaca ccaaactctc catgtcgact cgctgcaagg gtacaggaaa accatgcagt 180

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aggattgcgt ataactgctg caccggttct tgcagatcag gtaaagtgtg ctgatccagt 240  
 gcctgatctt ccccttctg tgctctatcc tttttctgcc tgagtcctcc ttacctgaga 300  
 gtggatcatga accactca 318

<210> 190  
 <211> 71  
 <212> PRT  
 <213> Conus magus

<400> 190  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30

Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Gly  
 35 40 45

Thr Gly Lys Pro Cys Ser Arg Ile Ala Tyr Asn Cys Cys Thr Gly Ser  
 50 55 60

Cys Arg Ser Gly Lys Cys Gly  
 65 70

<210> 191  
 <211> 25  
 <212> PRT  
 <213> Conus magus

<220>  
 <221> PEPTIDE  
 <222> (1)..(25)  
 <223> Xaa at residue 7 is Pro or Hyp; Xaa at residue 13 is Tyr, 125I-Ty  
 r, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 191  
 Cys Lys Gly Thr Gly Lys Xaa Cys Ser Arg Ile Ala Xaa Asn Cys Cys  
 1 5 10 15

Thr Gly Ser Cys Arg Ser Gly Lys Cys  
 20 25

<210> 192  
 <211> 259  
 <212> DNA  
 <213> Conus magus

<400> 192  
 accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60  
 acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgcctg 120  
 aagtcggaca ccaaactctc catgttaact ttgcgctgcg catcttacgg aaaaccttgt 180  
 ggtatttaca acgactgctg caatacatgc gatccagcca gaaagacatg tacgtagctg 240  
 atccggcgctc tgatcttcc 259

<210> 193  
 <211> 72  
 <212> PRT

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<213> Conus magus

<400> 193

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
20 25 30

Ala Leu Lys Ser Asp Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Ala  
35 40 45

Ser Tyr Gly Lys Pro Cys Gly Ile Tyr Asn Asp Cys Cys Asn Thr Cys  
50 55 60

Asp Pro Ala Arg Lys Thr Cys Thr  
65 70

<210> 194

<211> 26

<212> PRT

<213> Conus magus

<220>

<221> PEPTIDE

<222> (1)..(26)

<223> Xaa at residue 7 and 20 is Pro or Hyp; Xaa at residue 4 and 11 is  
Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-pho  
spho-Ty

<400> 194

Cys Ala Ser Xaa Gly Lys Xaa Cys Gly Ile Xaa Asn Asp Cys Cys Asn  
1 5 10 15

Thr Cys Asp Xaa Ala Arg Lys Thr Cys Thr  
20 25

<210> 195

<211> 254

<212> DNA

<213> Conus magus

<400> 195

gaattttcag catcaccaaa accatcatca aaatgaaact gacgtgtgtg gtgatcgctcg 60

ccgtgctgct cctgacggcc tgtcaactca tcacagctga tgactccaga ggtacgcaga 120

agcatcgtgc cctgaggtcg gacaccaaac tctccatgtc aactcgctgc aagggtaaag 180

gagcatcatg tcataggact tcgtatgact gctgcaccgg ttcttgcaac agaggtaaag 240

ttggctgata cgcc 254

<210> 196

<211> 71

<212> PRT

<213> Conus magus

<400> 196

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
20 25 30

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Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Gly  
                   35                                  40  45

Lys Gly Ala Ser Cys His Arg Thr Ser Tyr Asp Cys Cys Thr Gly Ser  
           50  55  60

Cys Asn Arg Gly Lys Phe Gly  
   65  70

<210> 197  
 <211> 25  
 <212> PRT  
 <213> Conus magus

<220>  
 <221> PEPTIDE  
 <222> (1)---(25)

<223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 197  
 Cys Lys Gly Lys Gly Ala Ser Cys His Arg Thr Ser Xaa Asp Cys Cys  
   1                                  5  10  15

Thr Gly Ser Cys Asn Arg Gly Lys Cys  
                   20  25

<210> 198  
 <211> 358  
 <212> DNA  
 <213> Conus miles

<400> 198  
 ggatccatga aactgacgtg cgtggtgatc atcgccatgc tgttcctgac agcctatcaa 60  
 ctgcgtacag ctgcgagcta cgccaaagggt aaacagaagc atcgtgctct gaggccagct 120  
 gacaaacacc tcagggttgac caagcgttgc aatgatcgcg gtggagggttg cagtcaacat 180  
 cctcactgct gcggtggaac ttgcaataag cttattggcg tatgtctgta aagctggtct 240  
 gccgtctgat attccctttc tgtgcttcat cctcttttgc ctgagtcatc catacctgtg 300  
 aatgggtaag agccactcaa tacctattcc tctggggggt tcagaggaac tactttac 358

<210> 199  
 <211> 74  
 <212> PRT  
 <213> Conus miles

<400> 199  
 Met Lys Leu Thr Cys Val Val Ile Ile Ala Met Leu Phe Leu Thr Ala  
   1                                  5  10  15  
 Tyr Gln Leu Ala Thr Ala Ala Ser Tyr Ala Lys Gly Lys Gln Lys His  
                   20  25  30  
 Arg Ala Leu Arg Pro Ala Asp Lys His Leu Arg Leu Thr Lys Arg Cys  
           35  40  45  
 Asn Asp Arg Gly Gly Gly Cys Ser Gln His Pro His Cys Cys Gly Gly  
   50  55  60  
 Thr Cys Asn Lys Leu Ile Gly Val Cys Leu  
   65  70

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<210> 200  
 <211> 27  
 <212> PRT  
 <213> Conus arenatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(27)  
 <223> Xaa at residue 12 is Pro or Hyp

<400> 200  
 Cys Asn Asp Arg Gly Gly Gly Cys Ser Gln His Xaa His Cys Cys Gly  
 1 5 10 15

Gly Thr Cys Asn Lys Leu Ile Gly Val Cys Leu  
 20 25

<210> 201  
 <211> 292  
 <212> DNA  
 <213> Conus monachus

<400> 201  
 accaaaaacca tcatcaaaat gaaactgacg agtgtggtga tcgtcgccgt gctgctcctg 60  
 acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccctg 120  
 aggtcggaca ccaaactctc catatcgact cgctgcaagt ctacaggaaa atcatgcagt 180  
 aggattgcgt ataactgctg caccggttct tgcagatcag gttaaattgtg ctgatccagc 240  
 gcctgatctt ccccttctg tgctctatcc ttttctgcct gagtcctcct ta 292

<210> 202  
 <211> 71  
 <212> PRT  
 <213> Conus monachus

<400> 202  
 Met Lys Leu Thr Ser Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30

Ala Leu Arg Ser Asp Thr Lys Leu Ser Ile Ser Thr Arg Cys Lys Ser  
 35 40 45

Thr Gly Lys Ser Cys Ser Arg Ile Ala Tyr Asn Cys Cys Thr Gly Ser  
 50 55 60

Cys Arg Ser Gly Lys Cys Gly  
 65 70

<210> 203  
 <211> 25  
 <212> PRT  
 <213> Conus monachus

<220>  
 <221> PEPTIDE  
 <222> (1)..(25)  
 <223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O  
 -sulpho-Tyr or O-phospho-Ty

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&lt;400&gt; 203

Cys Lys Ser Thr Gly Lys Ser Cys Ser Arg Ile Ala Xaa Asn Cys Cys  
 1 5 10 15

Thr Gly Ser Cys Arg Ser Gly Lys Cys  
 20 25

&lt;210&gt; 204

&lt;211&gt; 258

&lt;212&gt; DNA

&lt;213&gt; Conus monachus

&lt;400&gt; 204

acaaaaacca tcatcaaat gaaactgacg agtgtggtga tcgtcgccgt gctgctcctg 60

acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccctg 120

aggtcggaca ccaacctctc catgtcgact cgctgcaagg gtaaaggatc ttcatgtagt 180

aggaccatgt ataactgctg caccggttct tgcaacagag gtaaattgtg ctgatccagc 240

gcctgatctt ccccttc 258

&lt;210&gt; 205

&lt;211&gt; 71

&lt;212&gt; PRT

&lt;213&gt; Conus monachus

&lt;400&gt; 205

Met Lys Leu Thr Ser Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30

Ala Leu Arg Ser Asp Thr Asn Leu Ser Met Ser Thr Arg Cys Lys Gly  
 35 40 45

Lys Gly Ser Ser Cys Ser Arg Thr Met Tyr Asn Cys Cys Thr Gly Ser  
 50 55 60

Cys Asn Arg Gly Lys Cys Gly  
 65 70

&lt;210&gt; 206

&lt;211&gt; 25

&lt;212&gt; PRT

&lt;213&gt; Conus monachus

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(25)

<223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

&lt;400&gt; 206

Cys Lys Gly Lys Gly Ser Ser Cys Ser Arg Thr Met Xaa Asn Cys Cys  
 1 5 10 15

Thr Gly Ser Cys Asn Arg Gly Lys Cys  
 20 25

&lt;210&gt; 207

&lt;211&gt; 258

091008.02301

<212> DNA  
<213> Conus obscurus

<400> 207  
ctctctctct ctctgctgga caggctgcct cctgcatga aaggcggatc gtcatgccgc 60  
gggtactacgg gagtctgttg cggtttttgc agtgatttcg gctataaatg tagggactat 120  
ccccaaaact gatcttcccc cttctgtgct ctatcctttt ctgtccgagt cctcctgacc 180  
tgagagtggg catgaaccac tcatcaccta cccctctggg gcttcacagg atctacattg 240  
aaataaaaagc cgcattgc 258

<210> 208  
<211> 39  
<212> PRT  
<213> Conus obscurus

<400> 208  
Leu Leu Asp Arg Ser Pro Pro Cys Met Lys Gly Gly Ser Ser Cys Arg  
1 5 10 15  
Gly Thr Thr Gly Val Cys Cys Gly Phe Cys Ser Asp Phe Gly Tyr Lys  
20 25 30  
Cys Arg Asp Tyr Pro Gln Asn  
35

<210> 209  
<211> 35  
<212> PRT  
<213> Conus obscurus

<220>  
<221> PEPTIDE  
<222> (1)..(35)  
<223> Xaa at residue 2, 3 and 33 is Pro or Hyp; Xaa at residue 27 and 32 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 209  
Ser Xaa Xaa Cys Met Lys Gly Gly Ser Ser Cys Arg Gly Thr Thr Gly  
1 5 10 15  
Val Cys Cys Gly Phe Cys Ser Asp Phe Gly Xaa Lys Cys Arg Asp Xaa  
20 25 30  
Xaa Gln Asn  
35

<210> 210  
<211> 259  
<212> DNA  
<213> Conus obscurus

<400> 210  
ctctctctct ctctgctgga caggctgcact cgctgcttgc ctgacggaac gtcttgccctt 60  
tttagtagga tcagatgctg cggctacttgc agttcaatct taaagtcagtg tgtgagctga 120  
tccagcgggt gatcttcttc cctctgtgct ccatacctttt ctgcctgagt tctccttacc 180  
tgagagtggg catgaaccac tcatcaccta ctcttcttggg ggcttcagag gagctacatt 240

0910082 072301

gaaataaaaag ccgcattgc

<210> 211  
 <211> 32  
 <212> PRT  
 <213> Conus obscurus

<400> 211  
 Arg Ser Thr Arg Cys Leu Pro Asp Gly Thr Ser Cys Leu Phe Ser Arg  
 1 5 10 15  
 Ile Arg Cys Cys Gly Thr Cys Ser Ser Ile Leu Lys Ser Cys Val Ser  
 20 25 30

<210> 212  
 <211> 28  
 <212> PRT

<213> Conus monachus

<220>  
 <221> PEPTIDE  
 <222> (1)..(28)  
 <223> Xaa at residue 3 is Pro or Hyp

<400> 212  
 Cys Leu Xaa Asp Gly Thr Ser Cys Leu Phe Ser Arg Ile Arg Cys Cys  
 1 5 10 15

Gly Thr Cys Ser Ser Ile Leu Lys Ser Cys Val Ser  
 20 25

<210> 213  
 <211> 330  
 <212> DNA  
 <213> Conus pulicarius

<220>  
 <221> misc\_feature  
 <222> (1)..(330)  
 <223> n may be any nucleotide

<400> 213  
 atgaaactga cgtgtgtggt gatcatcgcc gtgctgttcc tgacggcctg tcaactcatt 60  
 acagctgaga cttactccag aggtaagcag aagcaccgtg ctttgagggtc aactgacaaa 120  
 aactccaagt tgactaggca gtgctcgctt aacgggtggat cttgttctcg tcattttcac 180  
 tgctgcagcc tctattgcaa taaaaatact ggcgtatgta ttgcaaccta ataccgtgt 240  
 gtgggtcatga accactcaat accctctcct ctggaggctt cagaggaact gcattgaaat 300  
 aaaactgcat tgcnttgacc aaaaaaaaaa 330

<210> 214  
 <211> 76  
 <212> PRT  
 <213> Conus pulicarius

<400> 214  
 Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15  
 Cys Gln Leu Ile Thr Ala Glu Thr Tyr Ser Arg Gly Lys Gln Lys His  
 20 25 30

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Arg Ala Leu Arg Ser Thr Asp Lys Asn Ser Lys Leu Thr Arg Gln Cys  
35 40 45

Ser Pro Asn Gly Gly Ser Cys Ser Arg His Phe His Cys Cys Ser Leu  
50 55 60

Tyr Cys Asn Lys Asn Thr Gly Val Cys Ile Ala Thr  
65 70 75

<210> 215  
<211> 30  
<212> PRT  
<213> Conus pulicarius

<220>  
<221> PEPTIDE  
<222> (1)..(30)  
<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 4 is Pro or H  
yp; Xaa at residue 19 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Ty  
r, O-sulpho-Tyr or O-phospho-Ty

<400> 215  
Xaa Cys Ser Xaa Asn Gly Gly Ser Cys Ser Arg His Phe His Cys Cys  
1 5 10 15

Ser Leu Xaa Cys Asn Lys Asn Thr Gly Val Cys Ile Ala Thr  
20 25 30

<210> 216  
<211> 282  
<212> DNA  
<213> Conus purpurascens

<400> 216  
atgaaactga cgtgtgtggt gatcgtcgcc gtgctgttcc tgacggcctg tcaactcatc 60  
acagctgatg actccagacg tacgcagaag catcgtgccc tgaggctcgac caccaaaggc 120  
gccacgtcga atcgcccctg caagacaccc ggacgaaaat gttttccgca tcagaaggac 180  
tgctgcggtc gagcgtgcat catcacaata tgtccctgat cttccccctt ctgtgctgta 240  
tccttttctg cctgagtctc cttacctgag agtggtcatg aa 282

<210> 217  
<211> 72  
<212> PRT  
<213> Conus purpurascens

<400> 217  
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Arg Thr Gln Lys His Arg  
20 25 30

Ala Leu Arg Ser Thr Thr Lys Gly Ala Thr Ser Asn Arg Pro Cys Lys  
35 40 45

Thr Pro Gly Arg Lys Cys Phe Pro His Gln Lys Asp Cys Cys Gly Arg  
50 55 60

Ala Cys Ile Ile Thr Ile Cys Pro  
65 70

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<210> 218  
 <211> 27  
 <212> PRT  
 <213> Conus purpurascens

<220>  
 <221> PEPTIDE  
 <222> (1)..(27)  
 <223> Xaa at residue 1, 5, 11 and 27 is Pro or Hyp

<400> 218  
 Xaa Cys Lys Thr Xaa Gly Arg Lys Cys Phe Xaa His Gln Lys Asp Cys  
 1 5 10 15

Cys Gly Arg Ala Cys Ile Ile Thr Ile Cys Xaa  
 20 25

<210> 219  
 <211> 340  
 <212> DNA  
 <213> Conus purpurascens

<400> 219  
 accaaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60  
 acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccctg 120  
 aggtcgacca ccaaactctt cacgtcgaaa agctgcaagc ttcccggagc atattgtaat 180  
 gcagaagatt atgactgctg ccttagatgc aaagttggag gtacatgtgg ctgatccagt 240  
 gcctgatctt cccccttctg tgctctatcc ttttctgect gagtcctcct tacctaagag 300  
 tggatcatgaa ccactcatca cttctcctc tggaggcttc 340

<210> 220  
 <211> 71  
 <212> PRT  
 <213> Conus purpurascens

<400> 220  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30

Ala Leu Arg Ser Thr Thr Lys Leu Phe Thr Ser Lys Ser Cys Lys Leu  
 35 40 45

Pro Gly Ala Tyr Cys Asn Ala Glu Asp Tyr Asp Cys Cys Leu Arg Cys  
 50 55 60

Lys Val Gly Gly Thr Cys Gly  
 65 70

<210> 221  
 <211> 26  
 <212> PRT  
 <213> Conus purpurascens

<220>  
 <221> PEPTIDE

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<222> (1)..(26)  
 <223> Xaa at residue 12 is Glu or gamma-carboxy Glu; Xaa at residue 5 is Pro or Hyp; Xaa at residue 8 and 14 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 221  
 Ser Cys Lys Leu Xaa Gly Ala Xaa Cys Asn Ala Xaa Asp Xaa Asp Cys  
 1 5 10 15  
 Cys Leu Arg Cys Lys Val Gly Gly Thr Cys  
 20 25

<210> 222  
 <211> 317  
 <212> DNA  
 <213> Conus purpurascens

<400> 222  
 atgaaactga cgtgtgtggt gatcgtcgcc gtgctgttcc tgacggcctg tcaactcatc 60  
 acagctgatg actccagacg tacgcagaag catcgtgccc tgaggctcgac caccaaacgc 120  
 gccacgtcga atcgcccctg caagaaaacc ggacgaaaat gttttccgca tcagaaggac 180  
 tgctgcggtc gagcgtgcat catcacaata tgtccctgat cttccccctt ctgtgctgta 240  
 tccttttctg cctgagtcct ccttacctga gagtgggtcat gaaccactca tcaccttctc 300  
 ctctggaggc ttcagag 317

<210> 223  
 <211> 72  
 <212> PRT  
 <213> Conus purpurascens

<400> 223  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15  
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Arg Thr Gln Lys His Arg  
 20 25 30  
 Ala Leu Arg Ser Thr Thr Lys Arg Ala Thr Ser Asn Arg Pro Cys Lys  
 35 40 45  
 Lys Thr Gly Arg Lys Cys Phe Pro His Gln Lys Asp Cys Cys Gly Arg  
 50 55 60  
 Ala Cys Ile Ile Thr Ile Cys Pro  
 65 70

<210> 224  
 <211> 27  
 <212> PRT  
 <213> Conus purpurascens

<220>  
 <221> PEPTIDE  
 <222> (1)..(27)  
 <223> Xaa at residue 1, 11 and 27 is Pro or Hyp

<400> 224  
 Xaa Cys Lys Lys Thr Gly Arg Lys Cys Phe Xaa His Gln Lys Asp Cys  
 1 5 10 15

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Cys Gly Arg Ala Cys Ile Ile Thr Ile Cys Xaa  
20 25

<210> 225  
<211> 328  
<212> DNA  
<213> Conus radiatus

<400> 225  
gctgatgcct gatcttcacg gttcttccct gtctcctttg gcatcaccaa aaccatcatc 60  
aaaatgaaac tgacgtgtgt ggtgatcgtc gccgtgctgg tcttgacggc ctgtcaactc 120  
atcacagctg atgactccag aggtatgcag aaacatcatg ccttgggggc gatcagcagt 180  
ctctttaagt cgaccggtca tgggtgcaaa cccctcaaac gtcgttggtt caatgataaa 240  
gaatgctgca gcaaattttg caattcagtc cgaaagcagt gtggataaat ggctaaaaaa 300  
ctgaataaaa gccgcattgc aaaaaaaaa 328

<210> 226  
<211> 74  
<212> PRT  
<213> Conus radiatus

<400> 226  
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Val Leu Thr Ala  
1 5 10 15  
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Met Gln Lys His His  
20 25 30  
Ala Leu Gly Ser Ile Ser Ser Leu Phe Lys Ser Thr Arg His Gly Cys  
35 40 45  
Lys Pro Leu Lys Arg Arg Cys Phe Asn Asp Lys Glu Cys Cys Ser Lys  
50 55 60  
Phe Cys Asn Ser Val Arg Lys Gln Cys Gly  
65 70

<210> 227  
<211> 28  
<212> PRT  
<213> Conus radiatus

<220>  
<221> PEPTIDE  
<222> (1)..(28)  
<223> Xaa at residue 15 is Glu or gamma-carboxy Glu; Xaa at residue 5 is Pro or Hy

<400> 227  
His Gly Cys Lys Xaa Leu Lys Arg Arg Cys Phe Asn Asp Lys Xaa Cys  
1 5 10 15  
Cys Ser Lys Phe Cys Asn Ser Val Arg Lys Gln Cys  
20 25

<210> 228  
<211> 250  
<212> DNA  
<213> Conus radiatus

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<400> 228  
gaaatgaaac tgacgtgtgt ggtgatcgtc gccgtgctgg tcctgacggc ctgtcaactc 60  
atcacagctg atgactccag aggtatgcag aaacatcatg ccctggggtc gatcagcagt 120  
ctctttaagt cgacccgctg tggctgcaaa cccctcaaac gtcgttgttt caatgataaa 180  
gaatgctgca gcaaattttg caattcagtc cgaaaccagt gtggataaat ggctaaaaac 240  
tgaataaaaag 250

<210> 229  
<211> 74  
<212> PRT  
<213> Conus radiatus

<400> 229  
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Val Leu Thr Ala  
1 5 10 15  
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Met Gln Lys His His  
20 25 30  
Ala Leu Gly Ser Ile Ser Ser Leu Phe Lys Ser Thr Arg Arg Gly Cys  
35 40 45  
Lys Pro Leu Lys Arg Arg Cys Phe Asn Asp Lys Glu Cys Cys Ser Lys  
50 55 60  
Phe Cys Asn Ser Val Arg Asn Gln Cys Gly  
65 70

<210> 230  
<211> 28  
<212> PRT  
<213> Conus radiatus

<220>  
<221> PEPTIDE  
<222> (1)..(28)  
<223> Xaa at residue 15 is Glu or gamma-carboxy Glu; Xaa at residue 5 is Pro or Hy

<400> 230  
Arg Gly Cys Lys Xaa Leu Lys Arg Arg Cys Phe Asn Asp Lys Xaa Cys  
1 5 10 15  
Cys Ser Lys Phe Cys Asn Ser Val Arg Asn Gln Cys  
20 25

<210> 231  
<211> 435  
<212> DNA  
<213> Conus radiatus

<400> 231  
ggaattccgc ttgcacggcg aacctgactt catctttctt ccctgcctcc tttggcatca 60  
ccaaaaccat catcaaaatg aaactgacgt gtgtggtgat cgtcgccgtg ctggctctga 120  
cggcctgtca actcatcaca gctgatgact ccagaggtat gcagaagcat catgccctga 180  
ggtcgatcac caaactctcc ctgtcgactc gctgcaaacc tcccggatca ccatgtagag 240  
tttcttcgta taactgctgc tcttcttgca aatcatacaa caagaaatgt ggctgaactt 300

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ccccctctgt gctctatcct tttcctgccc gagtcctcca tacctgagag tagtcatgaa 360  
 ccactgatta cctactcctc tggagggcct cagaggagct actttgaaat aaaagcccgc 420  
 attgcaaaaa aaaaa 435

<210> 232  
 <211> 72  
 <212> PRT  
 <213> Conus radiatus

<400> 232  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Val Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Met Gln Lys His His  
 20 25 30

Ala Leu Arg Ser Ile Thr Lys Leu Ser Leu Ser Thr Arg Cys Lys Pro  
 35 40 45

Pro Gly Ser Pro Cys Arg Val Ser Ser Tyr Asn Cys Cys Ser Ser Cys  
 50 55 60

Lys Ser Tyr Asn Lys Lys Cys Gly  
 65 70

<210> 233  
 <211> 27  
 <212> PRT  
 <213> Conus radiatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(27)  
 <223> Xaa at residue 3, 4 and 7 is Pro or Hyp; Xaa at residue 13 and 22  
 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-  
 phospho-Ty

<400> 233  
 Cys Lys Xaa Xaa Gly Ser Xaa Cys Arg Val Ser Ser Xaa Asn Cys Cys  
 1 5 10 15

Ser Ser Cys Lys Ser Xaa Asn Lys Lys Cys Gly  
 20 25

<210> 234  
 <211> 392  
 <212> DNA  
 <213> Conus rattus

<400> 234  
 ggatccatga aactgacgtg catggtgatc atcgccgtgc tgttcctgac agcctgtcaa 60  
 ttcgatacag ctgcgagcta cgacaaaggt aagcagaaac ctctactct gaggccagct 120  
 gacaaacaca tcaggttgac caagcgttgc aatgctcgca atgatggttg cagtcaacat 180  
 tctcaatgct gcagtggatc ttgcaataag actgcaggcg tatgtctgta aagctggtct 240  
 gccgtctgat attccctttc tgtgctttat cctcttttgc ctgagtcac catacctgtg 300  
 aatggttaag agccactcaa tacctactcc tctgggggct tcagaggaac tacattaaat 360

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aaagccacat tgcaaaaaaa aaaaaaaaaa aa

392

<210> 235  
 <211> 74  
 <212> PRT  
 <213> Conus rattus

<400> 235  
 Met Lys Leu Thr Cys Met Val Ile Ile Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15  
 Cys Gln Phe Asp Thr Ala Ala Ser Tyr Asp Lys Gly Lys Gln Lys Pro  
 20 25 30  
 Pro Thr Leu Arg Pro Ala Asp Lys His Ile Arg Leu Thr Lys Arg Cys  
 35 40 45

Asn Ala Arg Asn Asp Gly Cys Ser Gln His Ser Gln Cys Cys Ser Gly  
 50 55 60

Ser Cys Asn Lys Thr Ala Gly Val Cys Leu  
 65 70

<210> 236  
 <211> 27  
 <212> PRT  
 <213> Conus rattus

<400> 236  
 Cys Asn Ala Arg Asn Asp Gly Cys Ser Gln His Ser Gln Cys Cys Ser  
 1 5 10 15

Gly Ser Cys Asn Lys Thr Ala Gly Val Cys Leu  
 20 25

<210> 237  
 <211> 395  
 <212> DNA  
 <213> Conus rattus

<400> 237  
 ggatccatga aactgacgtg cgtggtgatc atcgccgtgc tgttcctgac agcctgtcaa 60  
 ctgatgcag ctgcgagcta cgacaaaggt aagcagaaac ctctactct gaggccagct 120  
 gacaaacact tcaggttgat caagcgttgc aatgctcgca atagtgggtg cagtcaacat 180  
 cctcaatgct gcagtggatc ttgcaataag actgcaggcg tatgtctgta aagctggtct 240  
 gccgtctgat attccctttc tgtgctttat cctcttttgc ctgagtcac cttacactgtg 300  
 aatggttaag agccactcaa tacctactcc tctgggggct tcagaggaac tacattaaat 360  
 aaagccacat tgcaacgaaa aaaaaaaaaa aaaaa 395

<210> 238  
 <211> 74  
 <212> PRT  
 <213> Conus rattus

<400> 238  
 Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Asp Ala Ala Ala Ser Tyr Asp Lys Gly Lys Gln Lys Pro

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20 25 30

Pro Thr Leu Arg Pro Ala Asp Lys His Phe Arg Leu Ile Lys Arg Cys  
35 40 45

Asn Ala Arg Asn Ser Gly Cys Ser Gln His Pro Gln Cys Cys Ser Gly  
50 55 60

Ser Cys Asn Lys Thr Ala Gly Val Cys Leu  
65 70

<210> 239  
<211> 27  
<212> PRT  
<213> Conus rattus

<220>  
<221> PEPTIDE  
<222> (1)..(27)  
<223> Xaa at residue 12 is Pro or Hyp

<400> 239  
Cys Asn Ala Arg Asn Ser Gly Cys Ser Gln His Xaa Gln Cys Cys Ser  
1 5 10 15

Gly Ser Cys Asn Lys Thr Ala Gly Val Cys Leu  
20 25

<210> 240  
<211> 390  
<212> DNA  
<213> Conus rattus

<400> 240  
ggatccatga aactgacgtg tgtggtgata atcgccgtgc tgttcctgac agcctgtcaa 60  
ttcgatacag ctgcgagcta cgacaaaggt aagcagaaac ctctactct gaggccagct 120  
gacaaacact tcaggttgat caagcgttgc aatgctcgca atagtgggtg cagtcaacat 180  
cctcaatgct gcagtggatc ttgcaataag actttgggcg tatgtctgta aagctgggtct 240  
gccgtctgat attccctttc tgtgctttat cctcttttgc ctgagtcata catacctgtg 300  
aatggttaag agccactcaa tacctactcc tctgggggct tcagaggaac tacattaaat 360  
aaagccacat tgaaaaaaaa aaaaaaaaaa 390

<210> 241  
<211> 74  
<212> PRT  
<213> Conus rattus

<400> 241  
Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Cys Gln Phe Asp Thr Ala Ala Ser Tyr Asp Lys Gly Lys Gln Lys Pro  
20 25 30

Pro Thr Leu Arg Pro Ala Asp Lys His Phe Arg Leu Ile Lys Arg Cys  
35 40 45

Asn Ala Arg Asn Ser Gly Cys Ser Gln His Pro Gln Cys Cys Ser Gly  
50 55 60

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Ser Cys Asn Lys Thr Leu Gly Val Cys Leu  
65 70

<210> 242  
<211> 27  
<212> PRT  
<213> Conus rattus

<220>  
<221> PEPTIDE  
<222> (1)..(27)  
<223> Xaa at residue 12 is Pro or Hyp

<400> 242  
Cys Asn Ala Arg Asn Ser Gly Cys Ser Gln His Xaa Gln Cys Cys Ser  
1 5 10 15

Gly Ser Cys Asn Lys Thr Leu Gly Val Cys Leu  
20 25

<210> 243  
<211> 379  
<212> DNA  
<213> Conus stercusmuscarum

<400> 243  
acaaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60  
acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccttg 120  
aggtcgaaga ccaaactctc catgtcgact cgctgcaaga gtaaaggagc aaaatgttca 180  
aggcttatgt atgactgctg cagcggttct tgcagcggct acacaggtag atgtggctga 240  
tccagcgcct gatcttcccc cttctgtgct ctatcctttt ctgcctgggt cctccttacc 300  
tgagagtggg catgaaccac tcatcaccta ctctcttgga ggcctcagag gagttacaat 360  
gaaataaaaag ccgcattgc 379

<210> 244  
<211> 73  
<212> PRT  
<213> Conus stercusmuscarum

<400> 244  
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
20 25 30

Ala Leu Arg Ser Lys Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Ser  
35 40 45

Lys Gly Ala Lys Cys Ser Arg Leu Met Tyr Asp Cys Cys Ser Gly Ser  
50 55 60

Cys Ser Gly Tyr Thr Gly Arg Cys Gly  
65 70

<210> 245  
<211> 27  
<212> PRT

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<213> Conus stercusmuscarum

<220>

<221> PEPTIDE

<222> (1)..(27)

<223> Xaa at residue 13 and 23 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 245

Cys Lys Ser Lys Gly Ala Lys Cys Ser Arg Leu Met Xaa Asp Cys Cys  
1 5 10 15

Ser Gly Ser Cys Ser Gly Xaa Thr Gly Arg Cys  
20 25

<210> 246

<211> 35

<212> PRT

<213> Conus stercusmuscarum

<220>

<221> PEPTIDE

<222> (1)..(35)

<223> Xaa at residue 33 is Pro or Hyp; Xaa at residue 10, 21, 24 and 32 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 246

Thr Thr Ser Cys Met Gln Ala Gly Ser Xaa Cys Gly Ser Thr Thr Arg  
1 5 10 15

Ile Cys Cys Gly Xaa Cys Ala Xaa Phe Gly Lys Lys Cys Ile Asp Xaa  
20 25 30

Xaa Ser Asn  
35

<210> 247

<211> 380

<212> DNA

<213> Conus stercusmuscarum

<400> 247

accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60  
acgacctgtc aactcatcac agctgatgac tccagaggta cgcaggagca tcgtgccctg 120  
aggtcgaaga ccaaactctc catgttaact ttgcgctgcg catcttacgg aaaaccttgt 180  
ggtattgaca acgactgctg caatgcatgc gatccagcca gaaatatatg tacgtagctg 240  
atccggcgctc tgatcttccc ccttctgtgc tctatccttt tctgcctgag tctccttac 300  
ctgagagtgg tcatgaacca ctcatcatct actctcctgg aggcctcaga ggagctacaa 360  
tgaaataaaa gccgcattgc 380

<210> 248

<211> 72

<212> PRT

<213> Conus stercusmuscarum

<400> 248

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Thr  
1 5 10 15

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Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Glu His Arg  
20 25 30

Ala Leu Arg Ser Lys Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Ala  
35 40 45

Ser Tyr Gly Lys Pro Cys Gly Ile Asp Asn Asp Cys Cys Asn Ala Cys  
50 55 60

Asp Pro Ala Arg Asn Ile Cys Thr  
65 70

<210> 249

<211> 26

<212> PRT

<213> Conus stercusmuscarum

<220>

<221> PEPTIDE

<222> (1)..(26)

<223> Xaa at residue 7 and 20 is Pro or Hyp; Xaa at residue 4 is Tyr, 1  
25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 249

Cys Ala Ser Xaa Gly Lys Xaa Cys Gly Ile Asp Asn Asp Cys Cys Asn  
1 5 10 15

Ala Cys Asp Xaa Ala Arg Asn Ile Cys Thr  
20 25

<210> 250

<211> 388

<212> DNA

<213> Conus stercusmuscarum

<400> 250

ggatccatga aactgacgtg tgtggtgatt gtcgccgtgc tgctcctgac ggctgtgcaa 60  
ctcatcacag ctgatgactc cagaggtacg caggagcatc gtgccctgag gtccaagacc 120  
aaactctcca tgttaacttt gcgctgcgta tcttacggaa aaccttgtgg tattgacaac 180  
gactgctgca atgcatgcca tccagccaga aatatatgta cgtagctgat ccggcgtctg 240  
atcttccccc ttctgtgctc tctcttttc tgccctgggtc ctccttacct gagagtggtc 300  
atgaaccact catcacctac tcctctggag gcctcagagg agttacaatg aaataaaaagc 360  
cgcatcgtcaa aaaaaaaaaa aaaaaaaaaa 388

<210> 251

<211> 72

<212> PRT

<213> Conus stercusmuscarum

<400> 251

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Glu His Arg  
20 25 30

Ala Leu Arg Ser Lys Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Val

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35 40 45  
 Ser Tyr Gly Lys Pro Cys Gly Ile Asp Asn Asp Cys Cys Asn Ala Cys  
 50 55 60

Asp Pro Ala Arg Asn Ile Cys Thr  
 65 70

<210> 252  
 <211> 26  
 <212> PRT  
 <213> Conus stercusmuscarum

<220>  
 <221> PEPTIDE  
 <222> (1)..(26)  
 <223>

Xaa-at-residue 7 and 20 is Pro or Hyp; Xaa at residue 4 is Tyr, 1  
 25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 252  
 Cys Val Ser Xaa Gly Lys Xaa Cys Gly Ile Asp Asn Asp Cys Cys Asn  
 1 5 10 15  
 Ala Cys Asp Xaa Ala Arg Asn Ile Cys Thr  
 20 25

<210> 253  
 <211> 264  
 <212> DNA  
 <213> Conus striatus

<400> 253  
 accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60  
 acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgttcctg 120  
 aggtcgacca ccaaagtctc caaggcgact gactgcattg aagccggaaa ttattgcgga 180  
 cctactgtta tgaaaatctg ctgcggcttt tgcagtccat acagcaaaat atgtatgaac 240  
 tatcccaaaa attgatcttc cccc 264

<210> 254  
 <211> 78  
 <212> PRT  
 <213> Conus striatus

<400> 254  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15  
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30  
 Ser Leu Arg Ser Thr Thr Lys Val Ser Lys Ala Thr Asp Cys Ile Glu  
 35 40 45  
 Ala Gly Asn Tyr Cys Gly Pro Thr Val Met Lys Ile Cys Cys Gly Phe  
 50 55 60  
 Cys Ser Pro Tyr Ser Lys Ile Cys Met Asn Tyr Pro Lys Asn  
 65 70 75

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<210> 255  
 <211> 36  
 <212> PRT  
 <213> Conus striatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(36)  
 <223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 13, 25 and 34 is Pro or Hyp; Xaa at residue 10, 26 and 33 is Tyr, 125 I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 255  
 Ala Thr Asp Cys Ile Xaa Ala Gly Asn Xaa Cys Gly Xaa Thr Val Met  
 1 5 10 15

~~Lys Ile Cys Cys Gly Phe Cys Ser Xaa Xaa Ser Lys Ile Cys Met Asn~~  
 20 25 30

Xaa Xaa Lys Asn  
 35

<210> 256  
 <211> 233  
 <212> DNA  
 <213> Conus striatus

<400> 256  
 gtcgactcgc tgcaagctta aaggacaatc atgtcgtagg actatgtatg actgctgcag 60  
 cggttcttgc ggcaggagag gtaaatgtgg ctgatccagc gcctgatctc ccccttctg 120  
 tgctctatcc ttttctgcct gggctcctct tacctgagag tggatcatgaa ccaatcatca 180  
 cctactcctc tggaggcctc agaggagcta caatgaaata aaagccgcat tgc 233

<210> 257  
 <211> 30  
 <212> PRT  
 <213> Conus striatus

<400> 257  
 Ser Thr Arg Cys Lys Leu Lys Gly Gln Ser Cys Arg Arg Thr Met Tyr  
 1 5 10 15

Asp Cys Cys Ser Gly Ser Cys Gly Arg Arg Gly Lys Cys Gly  
 20 25 30

<210> 258  
 <211> 26  
 <212> PRT  
 <213> Conus striatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(26)  
 <223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 258  
 Cys Lys Leu Lys Gly Gln Ser Cys Arg Arg Thr Met Xaa Asp Cys Cys  
 1 5 10 15

Ser Gly Ser Cys Gly Arg Arg Gly Lys Cys  
 20 25

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<210> 259  
 <211> 310  
 <212> DNA  
 <213> Conus striatus

<400> 259  
 accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tctgctccgt gctgctcctg 60  
 acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tctgcccctg 120  
 aggtcggaca ccaaactctc catgtcgact cgctgcaagg ctgcaggaaa atcatgcagt 180  
 aggattgcgt ataactgctg caccggttct tgcagatcag gtaaatgcgg ctgatccagc 240  
 gctgatctt ccccttctg tgctctatcc ttcttgctg agtctcttta cctgagagtg 300  
 gtcatgaacc 310

<210> 260  
 <211> 71  
 <212> PRT  
 <213> Conus striatus

<400> 260  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15  
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30  
 Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Ala  
 35 40 45  
 Ala Gly Lys Ser Cys Ser Arg Ile Ala Tyr Asn Cys Cys Thr Gly Ser  
 50 55 60  
 Cys Arg Ser Gly Lys Cys Gly  
 65 70

<210> 261  
 <211> 25  
 <212> PRT  
 <213> Conus striatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(25)  
 <223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 261  
 Cys Lys Ala Ala Gly Lys Ser Cys Ser Arg Ile Ala Xaa Asn Cys Cys  
 1 5 10 15  
 Thr Gly Ser Cys Arg Ser Gly Lys Cys  
 20 25

<210> 262  
 <211> 256  
 <212> DNA  
 <213> Conus striatus

<400> 262

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accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60  
 acggcctgtc aactcatcac agctgatgac tccagaggta cgcaggagca tcgtgccctg 120  
 aggtcggaca ccaaactctc catgttaact ttgcgctgcg aatcttacgg aaaaccttgt 180  
 ggtatttaca acgactgctg caatgcatgc gatccagcca aaaagacatg tacgtagctg 240  
 atccggcgtc tgatct 256

<210> 263  
 <211> 72  
 <212> PRT  
 <213> Conus striatus

<400> 263

~~Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala~~  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Glu His Arg  
 20 25 30

Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Glu  
 35 40 45

Ser Tyr Gly Lys Pro Cys Gly Ile Tyr Asn Asp Cys Cys Asn Ala Cys  
 50 55 60

Asp Pro Ala Lys Lys Thr Cys Thr  
 65 70

<210> 264  
 <211> 26  
 <212> PRT  
 <213> Conus striatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(26)  
 <223> Xaa at residue 2 is Glu or gamma-carboxy Glu; Xaa at residue 7 and  
 d 20 is Pro or Hyp; Xaa at residue 4 and 11 is Tyr, 125I-Tyr, mon  
 o-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 264

Cys Xaa Ser Xaa Gly Lys Xaa Cys Gly Ile Xaa Asn Asp Cys Cys Asn  
 1 5 10 15

Ala Cys Asp Xaa Ala Lys Lys Thr Cys Thr  
 20 25

<210> 265  
 <211> 229  
 <212> DNA  
 <213> Conus striatus

<400> 265

tctaggtcct ccggcagccc ctgtggtgtt actagtatat gctgtggtag atgctatagg 60  
 ggtaaagtga cgtagctcat cgggcgtctg atcttcccc ttctgtgctc catccttttc 120  
 tgctgagtc ctccttacct gagagtggtc gtgaaccact catcgctac tcctctggag 180  
 gcttcagagg ggctacacta aaataaaagc tatattgcaa tgaaaaaaa 229

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<210> 266  
 <211> 24  
 <212> PRT  
 <213> Conus striatus

<400> 266  
 Cys Arg Ser Ser Gly Ser Pro Cys Gly Val Thr Ser Ile Cys Cys Gly  
 1 5 10 15  
 Arg Cys Tyr Arg Gly Lys Cys Thr  
 20

<210> 267  
 <211> 24  
 <212> PRT  
 <213> Conus striatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(24)  
 <223> Xaa at residue 7 is Pro or Hyp; Xaa at residue 19 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 267  
 Cys Arg Ser Ser Gly Ser Xaa Cys Gly Val Thr Ser Ile Cys Cys Gly  
 1 5 10 15  
 Arg Cys Xaa Arg Gly Lys Cys Thr  
 20

<210> 268  
 <211> 26  
 <212> PRT  
 <213> Conus striatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(26)  
 <223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 268  
 Cys Lys Leu Lys Gly Gln Ser Cys Arg Lys Thr Ser Xaa Asp Cys Cys  
 1 5 10 15  
 Ser Gly Ser Cys Gly Arg Ser Gly Lys Cys  
 20 25

<210> 269  
 <211> 292  
 <212> DNA  
 <213> Conus striolatus

<400> 269  
 accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgtctt gctgctcctg 60  
 acgacctgtc gtctcatcac agctgatgac tccagaggta cgcagaagca tcgttcctg 120  
 aggtcgacta ctaaagtctc catgtcgact cgctgcaagg gtaaaggagc atcatgtctt 180  
 aggactgcgt atgactgctg caccggttct tgcaacagag gtagatgtgg ctgatccagc 240  
 gtctgatctt ccccttctg tgctctatcc ttttctgctt gagtcctcct ta 292

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<210> 270  
 <211> 71  
 <212> PRT  
 <213> Conus striolatus

<400> 270  
 Met Lys Leu Thr Cys Val Val Ile Val Val Leu Leu Leu Leu Thr Thr  
 1 5 10 15  
 Cys Arg Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30  
 Ser Leu Arg Ser Thr Thr Lys Val Ser Met Ser Thr Arg Cys Lys Gly  
 35 40 45  
 Lys Gly Ala Ser Cys Leu Arg Thr Ala Tyr Asp Cys Cys Thr Gly Ser  
 50 55 60

Cys Asn Arg Gly Arg Cys Gly  
 65 70

<210> 271  
 <211> 25  
 <212> PRT  
 <213> Conus striolatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(25)  
 <223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O  
 -sulpho-Tyr or O-phospho-Ty

<400> 271  
 Cys Lys Gly Lys Gly Ala Ser Cys Leu Arg Thr Ala Xaa Asp Cys Cys  
 1 5 10 15  
 Thr Gly Ser Cys Asn Arg Gly Arg Cys  
 20 25

<210> 272  
 <211> 259  
 <212> DNA  
 <213> Conus striolatus

<400> 272  
 accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt tctgctgacg 60  
 gcgtgtcaac tcatcacagc tgaggactcc agaggtagac agaagcatcg taccctgagg 120  
 tcgaccgtca gacgctccaa gtccgagttg actacgagat gcaggccttc aggatccaac 180  
 tgttgtaata ttagtatctg ctgtggtaga tgcgttaaca gaagatgtac gtagctcatc 240  
 gggcgtctga tctttcccc 259

<210> 273  
 <211> 71  
 <212> PRT  
 <213> Conus striolatus

<400> 273  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Thr Ala Cys  
 1 5 10 15  
 Gln Leu Ile Thr Ala Glu Asp Ser Arg Gly Thr Gln Lys His Arg Thr

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20 25 30  
 Leu Arg Ser Thr Val Arg Arg Ser Lys Ser Glu Leu Thr Thr Arg Cys  
           35                  40                  45  
 Arg Pro Ser Gly Ser Asn Cys Gly Asn Ile Ser Ile Cys Cys Gly Arg  
           50                  55                  60  
 Cys Val Asn Arg Arg Cys Thr  
           65                  70

<210> 274  
 <211> 24  
 <212> PRT  
 <213> Conus striolatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(24)  
 <223> Xaa at residue 3 is Pro or Hyp

<400> 274  
 Cys Arg Xaa Ser Gly Ser Asn Cys Gly Asn Ile Ser Ile Cys Cys Gly  
   1                  5                  10                  15  
 Arg Cys Val Asn Arg Arg Cys Thr  
                   20

<210> 275  
 <211> 280  
 <212> DNA  
 <213> Conus striolatus

<400> 275  
 accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt tctgttcctg 60  
 acggcggtgc aactcatcac agctgaggac tccagaggta cacagaagca tcgttcctg 120  
 aggtcgacta ccaaagtctc caagtcgact agctgcatga aagccgggtc ttattgcgtc 180  
 gctactacga gaatctgctg cggttattgc gcttatttcg gcaaaatatg tattgactat 240  
 cccaaaaact gatcttcccc ctactgtgct ctatcctttt 280

<210> 276  
 <211> 77  
 <212> PRT  
 <213> Conus striolatus

<400> 276  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala  
   1                  5                  10                  15  
 Cys Gln Leu Ile Thr Ala Glu Asp Ser Arg Gly Thr Gln Lys His Arg  
           20                  25                  30  
 Ser Leu Arg Ser Thr Thr Lys Val Ser Lys Ser Thr Ser Cys Met Lys  
           35                  40                  45  
 Ala Gly Ser Tyr Cys Val Ala Thr Thr Arg Ile Cys Cys Gly Tyr Cys  
           50                  55                  60  
 Ala Tyr Phe Gly Lys Ile Cys Ile Asp Tyr Pro Lys Asn  
   65                  70                  75

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<210> 277

<211> 35

<212> PRT

<213> Conus striolatus

<220>

<221> PEPTIDE

<222> (1)..(35)

<223> Xaa at residue 33 is Pro or Hyp; Xaa at residue 10, 21, 24 and 32 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 277

Ser Thr Ser Cys Met Lys Ala Gly Ser Xaa Cys Val Ala Thr Thr Arg  
1 5 10 15

Ile Cys Cys Gly Xaa Cys Ala Xaa Phe Gly Lys Ile Cys Ile Asp Xaa  
20 25 30

Xaa Lys Asn  
35

<210> 278

<211> 174

<212> DNA

<213> Conus textile

<400> 278

gttgactcgg tactgcacgc ctcatggagg acattgtggt tatcataatg actgctgcag 60

tcatcaatgc aatataaaca gaaataaatg tgagtagctg atctggcatc tgatctgtgc 120

tcttcttac ctgagagtgg tcatgaacca ctcatcacct actcctctgg aggc 174

<210> 279

<211> 31

<212> PRT

<213> Conus textile

<400> 279

Leu Thr Arg Tyr Cys Thr Pro His Gly Gly His Cys Gly Tyr His Asn  
1 5 10 15

Asp Cys Cys Ser His Gln Cys Asn Ile Asn Arg Asn Lys Cys Glu  
20 25 30

<210> 280

<211> 28

<212> PRT

<213> Conus textile

<220>

<221> PEPTIDE

<222> (1)..(28)

<223> Xaa at residue 28 is Glu or gamma-carboxy Glu; Xaa at residue 4 is Pro or Hyp; Xaa at residue 1 and 11 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 280

Xaa Cys Thr Xaa His Gly Gly His Cys Gly Xaa His Asn Asp Cys Cys  
1 5 10 15

Ser His Gln Cys Asn Ile Asn Arg Asn Lys Cys Xaa  
20 25

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<210> 281  
 <211> 28  
 <212> PRT  
 <213> Conus textile

<220>  
 <221> PEPTIDE  
 <222> (1)..(28)  
 <223> Xaa at residue 28 is Glu or gamma-carboxy Glu; Xaa at residue 4 is Pro or Hyp; Xaa at residue 1 and 11 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 281  
 Xaa Cys Thr Xaa Xaa Gly Gly His Cys Gly Xaa His Asn Asp Cys Cys  
 1 5 10 15

Ser His Gln Cys Asn Ile Asn Arg Asn Lys Cys Xaa  
 20 25

<210> 282  
 <211> 379  
 <212> DNA  
 <213> Conus tulipa

<400> 282  
 accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60  
 acggcctgtc agctcatcac agctctgcac tccagaggtg cgcagaagca tcgtgccctg 120  
 gggcggacca ccaaactcac cttgtcgact cgctgcaaat caccgggacg tccatgttca 180  
 ccgactagtt ataattgctg ctggtcttgc agtccataca gaaaaaaatg taggggctaa 240  
 tccagcgctt gattttcccc cttctgtgct ctattccttt ctgcctgagt cctccttacc 300  
 tgaaagtggg catgaaccac tcatcaccta cttctctgga ggcttcggag gagctacatt 360  
 gaaataaaaag ccgcattgc 379

<210> 283  
 <211> 73  
 <212> PRT  
 <213> Conus tulipa

<400> 283  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Leu His Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30

Ala Leu Gly Arg Thr Thr Lys Leu Thr Leu Ser Thr Arg Cys Lys Ser  
 35 40 45

Pro Gly Ser Pro Cys Ser Pro Thr Ser Tyr Asn Cys Cys Trp Ser Cys  
 50 55 60

Ser Pro Tyr Arg Lys Lys Cys Arg Gly  
 65 70

<210> 284  
 <211> 27  
 <212> PRT  
 <213> Conus tulipa

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&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(27)

<223> Xaa at residue 3, 7, 10 and 21 is Pro or Hyp; Xaa at residue 17 is Trp or Bromo Trp; Xaa at residue 13 and 22 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

&lt;400&gt; 284

Cys Lys Ser Xaa Gly Ser Xaa Cys Ser Xaa Thr Ser Xaa Asn Cys Cys  
1 5 10 15

Xaa Ser Cys Ser Xaa Xaa Arg Lys Lys Cys Arg  
20 25

&lt;210&gt; 285

&lt;211&gt; 379

&lt;212&gt; DNA

&lt;213&gt; Conus tulipa

&lt;400&gt; 285

acaaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60  
acggcctgtc agctcatcac agctctgcac tccagaggtg cgcagaagca tcgtgccctg 120  
gggtcgacca ccaaactcac cttgtcgact cgctgcttgt caccgggacg ttcattgttca 180  
ccgactagtt ataattgctg caggtcttgc aatccatata gcagaaaatg taggggctaa 240  
tccagcgcct gatcttcccc cttctgtgct ctattccttt ctgcttgagt cctccttacc 300  
tgaaagtggg catgaaccac tcatcaccta cttctctgga ggcttcggag gagctacatt 360  
gaaataaaaag ccgcattgc 379

&lt;210&gt; 286

&lt;211&gt; 73

&lt;212&gt; PRT

&lt;213&gt; Conus tulipa

&lt;400&gt; 286

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
1 5 10 15

Cys Gln Leu Ile Thr Ala Leu His Ser Arg Gly Thr Gln Lys His Arg  
20 25 30

Ala Leu Gly Ser Thr Thr Lys Leu Thr Leu Ser Thr Arg Cys Leu Ser  
35 40 45

Pro Gly Ser Ser Cys Ser Pro Thr Ser Tyr Asn Cys Cys Arg Ser Cys  
50 55 60

Asn Pro Tyr Ser Arg Lys Cys Arg Gly  
65 70

&lt;210&gt; 287

&lt;211&gt; 27

&lt;212&gt; PRT

&lt;213&gt; Conus tulipa

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(27)

<223> Xaa at residue 4, 10 and 21 is Pro or Hyp; Xaa at residue 13 and

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22 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 287

Cys Leu Ser Xaa Gly Ser Ser Cys Ser Xaa Thr Ser Xaa Asn Cys Cys  
1 5 10 15

Arg Ser Cys Asn Xaa Xaa Ser Arg Lys Cys Arg  
20 25

<210> 288

<211> 401

<212> DNA

<213> Conus viola

<400> 288

accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60  
acggcctgtc agctcattac agctgatgac tccagaggta cgcagttgca tcgtgccctg 120  
aggaaggcca ccaaactccc cgtgtcgact cgctgcatta ctttaggaac acgatgtaag 180  
gttccgagtc aatgctgcag atcttcttgc aagaacggtc gttgtgctcc atcccctgaa 240  
gaatggtaaa tgtggctgat ccagcgctg atcttcccc ttctgactgt ctccgacctt 300  
ttctgcctga gtctctctta cctgagaggt gtcataaacc actcatcacc tactcccctg 360  
gaagcttcag aggagctaca ttgaaataaa agccgcattg c 401

<210> 289

<211> 76

<212> PRT

<213> Conus viola

<400> 289

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Leu His Arg  
20 25 30

Ala Leu Arg Lys Ala Thr Lys Leu Pro Val Ser Thr Arg Cys Ile Thr  
35 40 45

Leu Gly Thr Arg Cys Lys Val Pro Ser Gln Cys Cys Arg Ser Ser Cys  
50 55 60

Lys Asn Gly Arg Cys Ala Pro Ser Pro Glu Glu Trp  
65 70 75

<210> 290

<211> 31

<212> PRT

<213> Conus viola

<220>

<221> PEPTIDE

<222> (1)..(31)

<223> Xaa at residue 29 and 30 is Glu or gamma-carboxy Glu; Xaa at residue 11, 26 and 28 is Pro or Hyp; Xaa at residue 31 is Trp or Brom o Tr

<400> 290

Cys Ile Thr Leu Gly Thr Arg Cys Lys Val Xaa Ser Gln Cys Cys Arg

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1              5              10              15
Ser Ser Cys Lys Asn Gly Arg Cys Ala Xaa Ser Xaa Xaa Xaa Xaa
      20              25              30
<210> 291
<211> 372
<212> DNA
<213> Conus viola

<400> 291
acaaaaacca tcataaaaat gaaactgacg tgtgtggtga tcgtgcgcgt gctgctcctg      60
acggcctgtc agctcattat agctggggac tccagaggta cgcagttgca tcgtgccctg      120
aggaaggcca ccaaactctc cgtgtcgaact cgtgtgcaaga-gtagaggatc atcatgtcgt      180
aggacttcgt atgactgctg cacgggttct tgcagaaatg gtaaagtgtg ctgatccagc      240
gcctgatctt ccccttcttg tgctccatcc ttttctgcct gagtctcctt tacctgagag      300
tgggcatgaa cactcatca cctactccct ggaagcttca gaggagctac attgaaataa      360
aagccgcatt gc
                                           372

<210> 292
<211> 71
<212> PRT
<213> Conus viola

<400> 292
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
1              5              10              15
Cys Gln Leu Ile Ile Ala Gly Asp Ser Arg Gly Thr Gln Leu His Arg
      20              25              30
Ala Leu Arg Lys Ala Thr Lys Leu Ser Val Ser Thr Arg Cys Lys Ser
      35              40              45
Arg Gly Ser Ser Cys Arg Arg Thr Ser Tyr Asp Cys Cys Thr Gly Ser
      50              55              60
Cys Arg Asn Gly Lys Cys Gly
      65              70

<210> 293
<211> 25
<212> PRT
<213> Conus viola

<220>
<221> PEPTIDE
<222> (1)..(25)
<223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O
      -sulpho-Tyr or O-phospho-Ty

<400> 293
Cys Lys Ser Arg Gly Ser Ser Cys Arg Arg Thr Ser Xaa Asp Cys Cys
1              5              10              15
Thr Gly Ser Cys Arg Asn Gly Lys Cys
      20              25

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<210> 294  
 <211> 380  
 <212> DNA  
 <213> Conus viola

<400> 294  
 accaaaaacca tcatcaaaat gaaactgacg tgtgtggcga tcgtcgccgt gctgctcctg 60  
 acggcctgtc agctcattac agctgaagac tccagaggta cgcattgagca ttttgccctg 120  
 aagtcgacct ccaaagtctc caagtcgact agctgcatgg aagccagatc ttattgcgga 180  
 cctgctacta cgaaaatctg ctgcgatttt tgcagtcocat tcagcgatag atgtatgaac 240  
 aatcccaaca attgatcttc ccccttgtgt gctccatctt ttctgcctga gtcctcctta 300  
 cctgagagtg gtcattgaacc actcatcacc tactcctctg gaggtctcag aggagttaca 360  
 ttgaaataaa agccgcatgc 380

<210> 295  
 <211> 78  
 <212> PRT  
 <213> Conus viola

<400> 295  
 Met Lys Leu Thr Cys Val Ala Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15  
 Cys Gln Leu Ile Thr Ala Glu Asp Ser Arg Gly Thr His Glu His Leu  
 20 25 30  
 Ala Leu Lys Ser Thr Ser Lys Val Ser Lys Ser Thr Ser Cys Met Glu  
 35 40 45  
 Ala Arg Ser Tyr Cys Gly Pro Ala Thr Thr Lys Ile Cys Cys Asp Phe  
 50 55 60  
 Cys Ser Pro Phe Ser Asp Arg Cys Met Asn Asn Pro Asn Asn  
 65 70 75

<210> 296  
 <211> 36  
 <212> PRT  
 <213> Conus viola

<220>  
 <221> PEPTIDE  
 <222> (1)..(36)  
 <223> Xaa at residue6 is Glu or gamma-carboxy Glu; Xaa at residue 13,  
 25 and 34 is Pro or Hyp; Xaa at residue 10 is Tyr, 125I-Tyr, mono  
 -iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 296  
 Ser Thr Ser Cys Met Xaa Ala Arg Ser Xaa Cys Gly Xaa Ala Thr Thr  
 1 5 10 15  
 Lys Ile Cys Cys Asp Phe Cys Ser Xaa Phe Ser Asp Arg Cys Met Asn  
 20 25 30  
 Asn Xaa Asn Asn  
 35

<210> 297  
 <211> 373

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&lt;212&gt; DNA

&lt;213&gt; Conus viola

&lt;400&gt; 297

accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60  
 acggcctgtc agctcattac agctgaggac tccagaggta cgcagttgca tcgtgccctg 120  
 aggaagacca ccaaactctc cttgtcgact cgctgcaagg gtccaggagc catatgtata 180  
 aggattgcgt ataactgctg caagtattct tgcggaaatg gtaaattgtg ctgatccagc 240  
 gcctgatctt cccccttgtg tgctccatcc tttttctgcc tgagtcctcc ttacctgaga 300  
 gtggtcatga accactcatc acctactcct ctggaggctt cagaggagct acattgaaat 360

aaaagccgca tgc

373

&lt;210&gt; 298

&lt;211&gt; 71

&lt;212&gt; PRT

&lt;213&gt; Conus viola

&lt;400&gt; 298

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Glu Asp Ser Arg Gly Thr Gln Leu His Arg  
 20 25 30

Ala Leu Arg Lys Thr Thr Lys Leu Ser Leu Ser Thr Arg Cys Lys Gly  
 35 40 45

Pro Gly Ala Ile Cys Ile Arg Ile Ala Tyr Asn Cys Cys Lys Tyr Ser  
 50 55 60

Cys Gly Asn Gly Lys Cys Gly  
 65 70

&lt;210&gt; 299

&lt;211&gt; 25

&lt;212&gt; PRT

&lt;213&gt; Conus viola

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(25)

<223> Xaa at residue 3 is Pro or Hyp; Xaa at residue 13 and 18 is Tyr,  
 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-T  
 y

&lt;400&gt; 299

Cys Lys Gly Xaa Gly Ala Ile Cys Ile Arg Ile Ala Xaa Asn Cys Cys  
 1 5 10 15

Lys Xaa Ser Cys Gly Asn Gly Lys Cys  
 20 25

&lt;210&gt; 300

&lt;211&gt; 353

&lt;212&gt; DNA

&lt;213&gt; Conus viola

&lt;400&gt; 300

accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgttctg 60

F06220"28001660

acggcctgtc aattcatcac agctgatgac tccagaagta cgcagaagca tcgtgccctg 120  
 aggtcgacca ccaaacactt tatgttgact tgggtactgca cgccttatgg aggacattgt 180  
 gggtattata atgactgctg cagtcacaa tgcaatataa acagaaataa atgtgagtag 240  
 ctgatccggc atctgatctg tgctcgccct aacctgagag tggcatgaa ccaactcatca 300  
 tctactcctc tggaggcttc agaggagcta catggaaata aaagccgcat tgc 353

<210> 301  
 <211> 73  
 <212> PRT  
 <213> Conus viola

---

<400> 301  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15  
 Cys Gln Phe Ile Thr Ala Asp Asp Ser Arg Ser Thr Gln Lys His Arg  
 20 25 30  
 Ala Leu Arg Ser Thr Thr Lys His Phe Met Leu Thr Trp Tyr Cys Thr  
 35 40 45  
 Pro Tyr Gly Gly His Cys Gly Tyr Tyr Asn Asp Cys Cys Ser His Gln  
 50 55 60  
 Cys Asn Ile Asn Arg Asn Lys Cys Glu  
 65 70

<210> 302  
 <211> 28  
 <212> PRT  
 <213> Conus viola

<220>  
 <221> PEPTIDE  
 <222> (1)..(28)  
 <223> Xaa at residue 28 is Glu or gamma-carboxy Glu; Xaa at residue 4 is  
 s Pro or Hyp; Xaa at residue 1, 5, 11 and 12 is Tyr, 125I-Tyr, mo  
 no-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 302  
 Xaa Cys Thr Xaa Xaa Gly Gly His Cys Gly Xaa Xaa Asn Asp Cys Cys  
 1 5 10 15  
 Ser His Gln Cys Asn Ile Asn Arg Asn Lys Cys Xaa  
 20 25

<210> 303  
 <211> 294  
 <212> DNA  
 <213> Conus pulicarius

<400> 303  
 ggatccatga aactgacgtg cgtggtgatt atcgccgtgc tgttcctgac ggctgtgcaa 60  
 ctcatcag ctgagactta ctccagaggt aagcagatgc accgtgctct gaggtcaact 120  
 gacaaaaact ccaagttgac cagggatgc acacctccag atggagcttg tggtttacct 180  
 acacactgct gcgggttttg cgatatggca aacaacagat gtctgtaaag cgtctgatat 240

09910032.072201

tccccttctg tgctctatcc tctttggcct gagtcatcca tacctgtgct cgag

294

<210> 304  
 <211> 73  
 <212> PRT  
 <213> Conus pulicarius

<400> 304  
 Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Glu Thr Tyr Ser Arg Gly Lys Gln Met His  
 20 25 30

Arg Ala Leu Arg Ser Thr Asp Lys Asn Ser Lys Leu Thr Arg Glu Cys  
 35 40 45

Thr Pro Pro Asp Gly Ala Cys Gly Leu Pro Thr His Cys Cys Gly Phe  
 50 55 60

Cys Asp Met Ala Asn Asn Arg Cys Leu  
 65 70

<210> 305  
 <211> 27  
 <212> PRT  
 <213> Conus pulicarius

<220>  
 <221> PEPTIDE  
 <222> (1)..(27)  
 <223> Xaa at residue 1 is Glu or gamma-carboxy Glu; Xaa at residue 4, 5  
 and 12 is Pro or Hy

<400> 305  
 Xaa Cys Thr Xaa Xaa Asp Gly Ala Cys Gly Leu Xaa Thr His Cys Cys  
 1 5 10 15

Gly Phe Cys Asp Met Ala Asn Asn Arg Cys Leu  
 20 25

<210> 306  
 <211> 294  
 <212> DNA  
 <213> Conus pulicarius

<400> 306  
 ggatccatga aactgacgtg cgtggtgatt atcgccgtgc tgttcttgac ggcctgtcaa 60  
 ctcattacag ctgagactta ctccagaggt aagcagatgc accgtgctct gaggtcaact 120  
 gacaaaaact ccagttgac cagggaatgc acacctccag gtggagcttg tggtttacct 180  
 acacactgct gcgggttttg cgatatggca aacaacagat gtctgtaaag cgtctgatat 240  
 tccccttctg tgctctatcc tctttggcct gagtcatcca tacctgtgct cgag 294

<210> 307  
 <211> 73  
 <212> PRT  
 <213> Conus pulicarius

<400> 307  
 Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

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Cys Gln Leu Ile Thr Ala Glu Thr Tyr Ser Arg Gly Lys Gln Met His  
20 25 30

Arg Ala Leu Arg Ser Thr Asp Lys Asn Ser Gln Leu Thr Arg Glu Cys  
35 40 45

Thr Pro Pro Gly Gly Ala Cys Gly Leu Pro Thr His Cys Cys Gly Phe  
50 55 60

Cys Asp Met Ala Asn Asn Arg Cys Leu  
65 70

<210> 308

<211> 27

<212> PRT

<213> Conus pulicarius

<220>

<221> PEPTIDE

<222> (1)..(27)

<223> Xaa at residue 1 is Glu or gamma-carboxy Glu; Xaa at residue 4, 5  
and 12 is Pro or Hy

<400> 308

Xaa Cys Thr Xaa Xaa Gly Gly Ala Cys Gly Leu Xaa Thr His Cys Cys  
1 5 10 15

Gly Phe Cys Asp Met Ala Asn Asn Arg Cys Leu  
20 25

<210> 309

<211> 307

<212> DNA

<213> Conus rattus

<400> 309

ggatccatga aactgacgtg tgtggtgatc atcgccgtgc tgttcctggc agcctgtcaa 60  
cctgttaca ctgagacttt ctccagaggt aaggagaagc gtcgtgctct gaggtcaact 120  
gacggcaact cccggttgac cagggcatgc acgcctgaag gtggagcctg tagtagtggg 180  
cgtcactgct gcggtctttg cgataacgtg tcccacacgt gctatggtga aacaccatct 240  
ctccactgat gtttcccctt ctgtgctcta tcttcttttg cctgagtcac ccatacctgt 300  
gctcgag 307

<210> 310

<211> 80

<212> PRT

<213> Conus rattus

<400> 310

Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Ala Ala  
1 5 10 15

Cys Gln Pro Val Thr Thr Glu Thr Phe Ser Arg Gly Lys Glu Lys Arg  
20 25 30

Arg Ala Leu Arg Ser Thr Asp Gly Asn Ser Arg Leu Thr Arg Ala Cys  
35 40 45

Thr Pro Glu Gly Gly Ala Cys Ser Ser Gly Arg His Cys Cys Gly Phe

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50 55 60  
 Cys Asp Asn Val Ser His Thr Cys Tyr Gly Glu Thr Pro Ser Leu His  
 65 70 75 80

<210> 311  
 <211> 34  
 <212> PRT  
 <213> Conus rattus

<220>  
 <221> PEPTIDE  
 <222> (1)..(34)  
 <223> Xaa at residue 5 and 29 is Glu or gamma-carboxy Glu; Xaa at residue 4 and 31 is Pro or Hyp; Xaa at residue 27 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 311  
 Ala Cys Thr Xaa Xaa Gly Gly Ala Cys Ser Ser Gly Arg His Cys Cys  
 1 5 10 15

Gly Phe Cys Asp Asn Val Ser His Thr Cys Xaa Gly Xaa Thr Xaa Ser  
 20 25 30

Leu His

<210> 312  
 <211> 342  
 <212> DNA  
 <213> Conus stercusmuscarum

<220>  
 <221> misc\_feature  
 <222> (1)..(342)  
 <223> n may be any nucleotide

<400> 312  
 agatccatga aactgacgtg cgtggtgata gtcgccgtgc tgctcctgac ggctgtgcaa 60  
 ctcatcacag ctgatgactc cagaggtacg caggagcatc gtgccctgag gtcggacacc 120  
 aaactcccca tatcgactcg ctgcaagggt aaaggagcat catgtcataa gactatgtat 180  
 gactgctgca gcggttctctg caccagaggt agatgtggct gatccagcgc ctgatcttcc 240  
 cccttctgtg ctctatcctt ttctgcctga gtcatacatc ctgtgctcga gcgttactag 300  
 tggatccgag ctcggtacca agcttggcgt aatcataaaa nc 342

<210> 313  
 <211> 71  
 <212> PRT  
 <213> Conus stercusmuscarum

<400> 313  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Glu His Arg  
 20 25 30

Ala Leu Arg Ser Asp Thr Lys Leu Pro Ile Ser Thr Arg Cys Lys Gly  
 35 40 45

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Lys Gly Ala Ser Cys His Lys Thr Met Tyr Asp Cys Cys Ser Gly Ser  
50 55 60

Cys Thr Arg Gly Arg Cys Gly  
65 70

<210> 314  
<211> 25  
<212> PRT  
<213> Conus stercusmuscarum

<220>  
<221> PEPTIDE  
<222> (1)..(25)  
<223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O  
-sulpho-Tyr or O-phospho-Ty

<400> 314  
Cys Lys Gly Lys Gly Ala Ser Cys His Lys Thr Met Xaa Asp Cys Cys  
1 5 10 15

Ser Gly Ser Cys Thr Arg Gly Arg Cys  
20 25

<210> 315  
<211> 33  
<212> PRT  
<213> Conus arenatus

<400> 315  
Gln Cys Ser Ala Asn Gly Gly Ser Cys Thr Arg His Phe His Cys Cys  
1 5 10 15

Ser Leu Tyr Cys Asn Lys Asp Ser Ser Val Cys Val Ala Thr Ser Tyr  
20 25 30

Pro

<210> 316  
<211> 28  
<212> PRT  
<213> Conus arenatus

<400> 316  
Thr Cys Asn Thr Pro Thr Glu Tyr Cys Thr Leu His Arg His Cys Cys  
1 5 10 15

Ser Gly Tyr Cys His Lys Thr Ile Gln Ala Cys Ser  
20 25

<210> 317  
<211> 33  
<212> PRT  
<213> Conus arenatus

<400> 317  
Gln Cys Thr Pro Asn Gly Gly Ser Cys Ser Arg His Phe His Cys Cys  
1 5 10 15

Ser Leu Tyr Cys Asn Lys Ser Thr Gly Val Cys Ile Ala Thr Ser Tyr  
20 25 30

Pro

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<210> 318  
 <211> 33  
 <212> PRT  
 <213> Conus arenatus

<400> 318  
 Gln Cys Thr Pro Asn Gly Gly Ser Cys Ser Arg His Phe His Cys Cys  
 1 5 10 15  
 Ser Leu Tyr Cys Asn Lys Ser Thr Gly Val Cys Ile Ala Thr Ser Tyr  
 20 25 30  
 Pro

<210> 319  
 <211> 27  
 <212> PRT  
 <213> Conus arenatus

<400> 319  
 Glu Cys Thr Pro Pro Gly Gly Ala Cys Gly Leu Pro Thr His Cys Cys  
 1 5 10 15  
 Gly Phe Cys Asp Thr Ala Asn Asn Arg Cys Leu  
 20 25

<210> 320  
 <211> 28  
 <212> PRT  
 <213> Conus arenatus

<400> 320  
 Thr Cys Asn Thr Pro Thr Glu Tyr Cys Thr Leu His Gln His Cys Cys  
 1 5 10 15  
 Ser Gly His Cys His Lys Thr Ile Gln Ala Cys Ala  
 20 25

<210> 321  
 <211> 30  
 <212> PRT  
 <213> Conus arenatus

<400> 321  
 Gln Cys Ser Pro Ile Gly Gly Tyr Cys Thr Leu His Ile His Cys Cys  
 1 5 10 15

Ser Asn His Cys Ile Lys Pro Ile Gly Arg Cys Val Ala Thr  
 20 25 30

<210> 322  
 <211> 30  
 <212> PRT  
 <213> Conus arenatus

<400> 322  
 Gln Cys Leu Pro Asn Gly Gly Tyr Cys Thr Leu His Ile His Cys Cys  
 1 5 10 15

Ser Asp His Cys Ile Lys Pro Ile Asp Arg Cys Val Ala Thr  
 20 25 30

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 100220-28001650

<210> 323  
 <211> 25  
 <212> PRT  
 <213> Conus aurisiacus

<400> 323  
 Cys Lys Gly Lys Gly Lys Pro Cys Ser Arg Ile Ser Tyr Asn Cys Cys  
 1 5 10 15  
 Thr Gly Ser Cys Arg Ser Gly Lys Cys  
 20 25

<210> 324  
 <211> 32  
 <212> PRT  
 <213> Conus aurisiacus

<400> 324  
 Cys Met Glu Ala Gly Ser Tyr Cys Gly Ser Thr Thr Arg Ile Cys Cys  
 1 5 10 15  
 Gly Phe Cys Ala Tyr Phe Gly Lys Lys Cys Ile Asp Tyr Pro Ser Asn  
 20 25 30

<210> 325  
 <211> 25  
 <212> PRT  
 <213> Conus aurisiacus

<400> 325  
 Cys Lys Ala Lys Gly Lys Pro Cys Ser Arg Ile Ala Tyr Asn Cys Cys  
 1 5 10 15  
 Thr Gly Ser Cys Arg Ser Gly Lys Cys  
 20 25

<210> 326  
 <211> 26  
 <212> PRT  
 <213> Conus aurisiacus

<400> 326  
 Cys Ala Ser Tyr Gly Lys Pro Cys Gly Ile Asp Asn Asp Cys Cys Asn  
 1 5 10 15  
 Ala Cys Asp Pro Gly Arg Asn Ile Cys Thr  
 20 25

<210> 327  
 <211> 36  
 <212> PRT  
 <213> Conus bullatus

<400> 327  
 Ser Thr Ser Cys Met Glu Ala Gly Ser Tyr Cys Gly Pro Ala Thr Thr  
 1 5 10 15  
 Lys Ile Cys Cys Asp Phe Cys Ser Pro Phe Ser Asp Arg Cys Met Asn  
 20 25 30

Asn Pro Asn Asn  
 35

<210> 328  
 <211> 31

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<212> PRT  
 <213> Conus bullatus

<400> 328  
 Cys Ile Thr Pro Gly Thr Arg Cys Lys Val Pro Ser Gln Cys Cys Arg  
 1 5 10 15  
 Gly Pro Cys Lys Asn Gly Arg Cys Thr Pro Ser Pro Ser Glu Trp  
 20 25 30

<210> 329  
 <211> 26  
 <212> PRT  
 <213> Conus bullatus

<400> 329  
 Cys Ala Thr Tyr Gly Lys Pro Cys Gly Ile Gln Asn Asp Cys Cys Asn  
 1 5 10 15

Thr Cys Asp Pro Ala Arg Arg Thr Cys Thr  
 20 25

<210> 330  
 <211> 25  
 <212> PRT  
 <213> Conus bullatus

<400> 330  
 Cys Lys Gly Pro Gly Ala Ser Cys Ile Arg Ile Ala Tyr Asn Cys Cys  
 1 5 10 15

Lys Tyr Ser Cys Arg Asn Gly Lys Cys  
 20 25

<210> 331  
 <211> 36  
 <212> PRT  
 <213> Conus bullatus

<400> 331  
 Ser Thr Ser Cys Met Ala Ala Gly Ser Tyr Cys Gly Pro Ala Thr Thr  
 1 5 10 15

Asn Ile Cys Cys Asp Phe Cys Ser Pro Phe Ser Asp Arg Cys Met Lys  
 20 25 30

Lys Pro Asn Asn  
 35

<210> 332  
 <211> 25  
 <212> PRT  
 <213> Conus bullatus

<400> 332  
 Cys Lys Ser Lys Gly Ser Ser Cys His Arg Thr Ser Tyr Asp Cys Cys  
 1 5 10 15

Thr Gly Ser Cys Arg Asn Gly Arg Cys  
 20 25

<210> 333  
 <211> 25  
 <212> PRT

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<213> Conus catus

<400> 333

Cys Lys Ser Thr Gly Ala Ser Cys Arg Arg Thr Ser Tyr Asp Cys Cys  
1 5 10 15

Thr Gly Ser Cys Arg Ser Gly Arg Cys  
20 25

<210> 334

<211> 25

<212> PRT

<213> Conus catus

<400> 334

Cys Gln Gly Arg Gly Ala Ser Cys Arg Lys Thr Met Tyr Asn Cys Cys  
1 5 10 15

Ser Gly Ser Cys Asn Arg Gly Ser Cys  
20 25

<210> 335

<211> 28

<212> PRT

<213> Conus catus

<400> 335

Cys Leu Pro Ala Gly Glu Ser Cys Leu Phe Ser Arg Ile Arg Cys Cys  
1 5 10 15

Gly Thr Cys Ser Ser Val Leu Lys Ser Cys Val Ser  
20 25

<210> 336

<211> 25

<212> PRT

<213> Conus catus

<400> 336

Cys Gln Gly Arg Gly Gly Pro Cys Thr Lys Ala Val Phe Asn Cys Cys  
1 5 10 15

Ser Gly Ser Cys Asn Arg Gly Arg Cys  
20 25

<210> 337

<211> 26

<212> PRT

<213> Conus catus

<400> 337

Cys Ala Thr Tyr Gly Lys Pro Cys Gly Ile Gln Asn Asp Cys Cys Asn  
1 5 10 15

Thr Cys Asp Pro Ala Arg Lys Thr Cys Thr  
20 25

<210> 338

<211> 25

<212> PRT

<213> Conus catus

<400> 338

Cys Arg Gly Arg Gly Gly Pro Cys Thr Lys Ala Met Phe Asn Cys Cys  
1 5 10 15

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Ser Gly Ser Cys Asn Arg Gly Arg Cys  
20 25

<210> 339  
<211> 33  
<212> PRT  
<213> Conus characteristicus

<400> 339  
Gln Cys Ser Ala Asn Gly Gly Ser Cys Thr Arg His Phe His Cys Cys  
1 5 10 15

Ser Leu Tyr Cys Asn Lys Asp Ser Ser Val Cys Val Ala Thr Ser Tyr  
20 25 30

Pro

<210> 340  
<211> 26  
<212> PRT  
<213> Conus consors

<400> 340  
Cys Ala Ser Tyr Gly Lys Pro Cys Gly Ile Asp Asn Asp Cys Cys Asn  
1 5 10 15

Thr Cys Asp Pro Ala Arg Lys Thr Cys Thr  
20 25

<210> 341  
<211> 25  
<212> PRT  
<213> Conus consors

<400> 341  
Cys Lys Gly Thr Gly Lys Pro Cys Ser Arg Ile Ala Tyr Asn Cys Cys  
1 5 10 15

Thr Gly Ser Cys Arg Ser Gly Lys Cys  
20 25

<210> 342  
<211> 36  
<212> PRT  
<213> Conus consors

<400> 342  
Ala Thr Asp Cys Ile Glu Ala Gly Asn Tyr Cys Gly Pro Thr Val Met  
1 5 10 15

Lys Ile Cys Cys Gly Phe Cys Ser Pro Tyr Ser Lys Ile Cys Met Asn  
20 25 30

Tyr Pro Gln Asn  
35

<210> 343  
<211> 27  
<212> PRT  
<213> Conus catus

<400> 343  
Cys Lys Gly Lys Gly Ala Ser Cys Thr Arg Leu Met Tyr Asp Cys Cys

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1                      5                      10                      15

His Gly Ser Cys Ser Ser Ser Lys Gly Arg Cys  
20                      25

<210> 344  
<211> 25  
<212> PRT  
<213> Conus consors

<400> 344  
Cys Lys Gly Lys Gly Ala Ser Cys His Arg Thr Ser Tyr Asp Cys Cys  
1                      5                      10                      15

Thr Gly Ser Cys Asn Arg Gly Lys Cys  
20                      25

<210> 345  
<211> 26  
<212> PRT  
<213> Conus consors

<400> 345  
Cys Ala Ser Tyr Gly Lys Pro Cys Gly Ile Tyr Asn Asp Cys Cys Asn  
1                      5                      10                      15

Thr Cys Asp Pro Ala Arg Lys Thr Cys Thr  
20                      25

<210> 346  
<211> 25  
<212> PRT  
<213> Conus consors

<400> 346  
Cys Lys Gly Thr Gly Lys Pro Cys Ser Arg Val Ala Tyr Asn Cys Cys  
1                      5                      10                      15

Thr Gly Ser Cys Arg Ser Gly Lys Cys  
20                      25

<210> 347  
<211> 35  
<212> PRT  
<213> Conus consors

<400> 347  
Ser Thr Ser Cys Met Lys Ala Gly Ser Tyr Cys Arg Ser Thr Thr Arg  
1                      5                      10                      15

Thr Cys Cys Gly Tyr Cys Ala Tyr Phe Gly Lys Phe Cys Ile Asp Phe  
20                      25                      30

Pro Ser Asn  
35

<210> 348  
<211> 25  
<212> PRT  
<213> Conus circumcişus

<400> 348  
Cys Lys Gly Lys Gly Ala Ser Cys Arg Lys Thr Met Tyr Asn Cys Cys  
1                      5                      10                      15

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Ser Gly Ser Cys Ser Asn Gly Arg Cys  
20 25

<210> 349  
<211> 35  
<212> PRT  
<213> Conus circumciscus

<400> 349  
Ser Thr Ser Cys Met Glu Ala Gly Ser Tyr Cys Arg Ser Thr Thr Arg  
1 5 10 15

Thr Cys Cys Gly Tyr Cys Ser Tyr Phe Ser Lys Lys Cys Ile Asp Phe  
20 25 30

Pro Ser Asn  
35

<210> 350  
<211> 27  
<212> PRT  
<213> Conus circumciscus

<400> 350  
Cys Lys Ser Lys Gly Ala Lys Cys Ser Arg Leu Met Tyr Asp Cys Cys  
1 5 10 15

Ser Gly Ser Cys Ser Arg Tyr Ser Gly Arg Cys  
20 25

<210> 351  
<211> 35  
<212> PRT  
<213> Conus circumciscus

<400> 351  
Ser Thr Gly Cys Met Lys Ala Gly Ser Tyr Cys Arg Ser Thr Thr Arg  
1 5 10 15

Thr Cys Cys Gly Tyr Cys Ala Tyr Phe Gly Lys Lys Cys Ile Asp Tyr  
20 25 30

Pro Ser Asn  
35

<210> 352  
<211> 28  
<212> PRT  
<213> Conus dalli

<400> 352  
Ser Cys Thr Pro Pro Gly Gly Pro Cys Gly Tyr Tyr Asn Asp Cys Cys  
1 5 10 15

Ser His Gln Cys Asn Ile Ser Arg Asn Lys Cys Glu  
20 25

<210> 353  
<211> 25  
<212> PRT  
<213> Conus distans

<220>  
<221> PEPTIDE

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<223> unknown *Conus* species

&lt;400&gt; 358

Cys Leu Ser Pro Gly Ser Arg Cys His Lys Thr Met Arg Asn Cys Cys  
 1 5 10 15

Thr Ser Cys Ser Ser Tyr Lys Gly Lys Cys Arg Pro Arg Lys  
 20 25 30

&lt;210&gt; 359

&lt;211&gt; 27

&lt;212&gt; PRT

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; unknown Conus species

&lt;400&gt; 359

Cys Lys Pro Pro Gly Arg Lys Cys Leu Asn Arg Lys Asn Glu Cys Cys  
 1 5 10 15

Ser Lys Phe Cys Asn Glu His Leu His Met Cys  
 20 25

&lt;210&gt; 360

&lt;211&gt; 26

&lt;212&gt; PRT

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; unknown Conus species

&lt;400&gt; 360

Cys Lys Pro Pro Arg Arg Lys Cys Leu Lys Ile Lys Asp Lys Cys Cys  
 1 5 10 15

Asn Phe Cys Asn Thr His Leu Asn Met Cys  
 20 25

&lt;210&gt; 361

&lt;211&gt; 28

&lt;212&gt; PRT

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; unknown Conus species

&lt;400&gt; 361

Cys Ala Gly Pro Gly Thr Ile Cys Pro Asn Arg Val Cys Cys Gly Tyr  
 1 5 10 15

Cys Ser Lys Arg Thr His Leu Cys His Ser Arg Thr  
 20 25

&lt;210&gt; 362

&lt;211&gt; 27

&lt;212&gt; PRT

&lt;213&gt; Conus laterculatus

&lt;400&gt; 362

Lys Cys Trp Pro Ser Gly Ser Tyr Cys Arg Ala Asn Ser Lys Cys Cys  
 1 5 10 15

Ser Gly Cys Asp Arg Asn Arg Asn Lys Cys Tyr  
 20 25

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<210> 363  
 <211> 27  
 <212> PRT  
 <213> Conus laterculatus

<400> 363  
 Cys Leu Pro Pro Gly Ser Tyr Cys Lys Ala Thr Thr Glu Val Cys Cys  
 1 5 10 15  
 Ser Ser Cys Leu Gln Phe Ala Gln Ile Cys Ser  
 20 25

<210> 364  
 <211> 30  
 <212> PRT  
 <213> Conus lynceus

<400> 364  
 Cys Lys Ser Pro Gly Ser Pro Cys Ser Val Thr Ser Tyr Asn Cys Cys  
 1 5 10 15  
 Thr Phe Cys Ser Ser Tyr Thr Lys Lys Cys Arg Ala Ser Leu  
 20 25 30

<210> 365  
 <211> 28  
 <212> PRT  
 <213> Conus lynceus

<400> 365  
 Cys Ala Gly Pro Gly Ala Ile Cys Pro Asn Arg Val Cys Cys Gly Tyr  
 1 5 10 15  
 Cys Ser Lys Arg Thr His Leu Cys His Ser Arg Thr  
 20 25

<210> 366  
 <211> 27  
 <212> PRT  
 <213> Conus lynceus

<400> 366  
 Ala Cys Trp Ser Ser Gly Thr Pro Cys Gly Thr Asp Ser Leu Cys Cys  
 1 5 10 15  
 Gly Gly Cys Asn Val Ser Lys Ser Lys Cys Asn  
 20 25

<210> 367  
 <211> 27  
 <212> PRT  
 <213> Conus lynceus

<400> 367  
 Lys Cys Trp Ser Pro Gly Thr Tyr Cys Arg Ala His Ser Lys Cys Cys  
 1 5 10 15  
 Arg Gly Cys Asp Gln Asn Arg Asn Lys Cys Tyr  
 20 25

<210> 368  
 <211> 29  
 <212> PRT  
 <213> Conus laterculatus

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<400> 368  
 Cys Lys Ser Pro Gly Ser Ser Cys Ser Val Ser Met Arg Asn Cys Cys  
 1 5 10 15

Thr Ser Cys Asn Ser Arg Thr Lys Lys Cys Thr Arg Arg  
 20 25

<210> 369  
 <211> 27  
 <212> PRT  
 <213> Conus laterculatus

<400> 369  
 Thr Cys Trp Pro Ser Gly Thr Ala Cys Gly Ile Asp Ser Asn Cys Cys  
 1 5 10 15

Ser Gly Cys Asn Val Ser Arg Ser Lys Cys Asn  
 20 25

<210> 370  
 <211> 27  
 <212> PRT  
 <213> Conus laterculatus

<400> 370  
 Lys Cys Trp Pro Ser Gly Ser Tyr Cys Arg Ala Asn Ser Lys Cys Cys  
 1 5 10 15

Ser Gly Cys Asp Arg Asn Arg Ser Lys Cys Asn  
 20 25

<210> 371  
 <211> 37  
 <212> PRT  
 <213> Conus leopardus

<400> 371  
 Ser Leu Phe Glu Cys Ala Pro Ser Gly Gly Arg Cys Gly Phe Leu Lys  
 1 5 10 15

Ser Cys Cys Glu Gly Tyr Cys Asp Gly Glu Ser Thr Ser Cys Val Ser  
 20 25 30

Gly Pro Tyr Ser Ile  
 35

<210> 372  
 <211> 30  
 <212> PRT  
 <213> Conus leopardus

<400> 372  
 Trp Pro Leu Asp Cys Thr Ala Pro Ser Gln Pro Cys Gly Tyr Phe Pro  
 1 5 10 15

Arg Cys Cys Gly His Cys Asp Val Arg Arg Val Cys Thr Ser  
 20 25 30

<210> 373  
 <211> 31  
 <212> PRT  
 <213> Conus leopardus

<400> 373  
 Cys Met Ser Pro Gly Gly Ile Cys Gly Asp Phe Gly Asp Cys Cys Glu

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1                      5                      10                      15  
 Ile Cys Asn Val Tyr Gly Ile Cys Val Ser Asp Leu Pro Gly Ile  
                     20                      25                      30

<210> 374  
 <211> 27  
 <212> PRT  
 <213> Conus leopardus

<400> 374  
 Tyr Cys Ala Pro Pro Gly Gly Ala Cys Gly Phe Phe Asp His Cys Cys  
 1                      5                      10                      15

Gly Tyr Cys Glu Thr Phe Tyr Asn Thr Cys Arg  
                     20                      25

<210> 375  
 <211> 25  
 <212> PRT  
 <213> Conus magus

<400> 375  
 Cys Lys Gly Thr Gly Lys Pro Cys Ser Arg Ile Ala Tyr Asn Cys Cys  
 1                      5                      10                      15

Thr Gly Ser Cys Arg Ser Gly Lys Cys  
                     20                      25

<210> 376  
 <211> 26  
 <212> PRT  
 <213> Conus magus

<400> 376  
 Cys Ala Ser Tyr Gly Lys Pro Cys Gly Ile Tyr Asn Asp Cys Cys Asn  
 1                      5                      10                      15

Thr Cys Asp Pro Ala Arg Lys Thr Cys Thr  
                     20                      25

<210> 377  
 <211> 27  
 <212> PRT  
 <213> Conus miles

<400> 377  
 Cys Asn Asp Arg Gly Gly Gly Cys Ser Gln His Pro His Cys Cys Gly  
 1                      5                      10                      15

Gly Thr Cys Asn Lys Leu Ile Gly Val Cys Leu  
                     20                      25

<210> 378  
 <211> 25  
 <212> PRT  
 <213> Conus monachus

<400> 378  
 Cys Lys Ser Thr Gly Lys Ser Cys Ser Arg Ile Ala Tyr Asn Cys Cys  
 1                      5                      10                      15

Thr Gly Ser Cys Arg Ser Gly Lys Cys  
                     20                      25

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<210> 379  
 <211> 25  
 <212> PRT  
 <213> *Conus monachus*

<400> 379  
 Cys Lys Gly Lys Gly Ser Ser Cys Ser Arg Thr Met Tyr Asn Cys Cys  
 1 5 10 15  
 Thr Gly Ser Cys Asn Arg Gly Lys Cys  
 20 25

<210> 380  
 <211> 35  
 <212> PRT  
 <213> *Conus obscurus*

<400> 380  
 Ser Pro Pro Cys Met Lys Gly Gly Ser Ser Cys Arg Gly Thr Thr Gly  
 1 5 10 15  
 Val Cys Cys Gly Phe Cys Ser Asp Phe Gly Tyr Lys Cys Arg Asp Tyr  
 20 25 30  
 Pro Gln Asn  
 35

<210> 381  
 <211> 28  
 <212> PRT  
 <213> *Conus obscurus*

<400> 381  
 Cys Leu Pro Asp Gly Thr Ser Cys Leu Phe Ser Arg Ile Arg Cys Cys  
 1 5 10 15  
 Gly Thr Cys Ser Ser Ile Leu Lys Ser Cys Val Ser  
 20 25

<210> 382  
 <211> 27  
 <212> PRT  
 <213> *Conus purpurascens*

<220>  
 <221> PEPTIDE  
 <222> (1)..(27)  
 <223> Xaa is Hyp

<400> 382  
 Xaa Cys Lys Thr Xaa Gly Arg Lys Cys Phe Xaa His Gln Lys Asp Cys  
 1 5 10 15  
 Cys Gly Arg Ala Cys Ile Ile Thr Ile Cys Pro  
 20 25

<210> 383  
 <211> 26  
 <212> PRT  
 <213> *Conus purpurascens*

<220>  
 <221> PEPTIDE  
 <222> (1)..(26)  
 <223> Xaa at residue 5 is Hyp; Xaa at residue 12 is gamma-carboxy-Glu

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&lt;400&gt; 383

Ser Cys Lys Leu Xaa Gly Ala Tyr Cys Asn Ala Xaa Asp Tyr Asp Cys  
 1 5 10 15

Cys Leu Arg Cys Lys Val Gly Gly Thr Cys  
 20 25

&lt;210&gt; 384

&lt;211&gt; 27

&lt;212&gt; PRT

&lt;213&gt; Conus purpurascens

&lt;400&gt; 384

Pro Cys Lys Lys Thr Gly Arg Lys Cys Phe Pro His Gln Lys Asp Cys  
 1 5 10 15

Cys Gly Arg Ala Cys Ile Ile Thr Ile Cys Pro  
 20 25

&lt;210&gt; 385

&lt;211&gt; 30

&lt;212&gt; PRT

&lt;213&gt; Conus pulicarius

&lt;400&gt; 385

Gln Cys Ser Pro Asn Gly Gly Ser Cys Ser Arg His Phe His Cys Cys  
 1 5 10 15

Ser Leu Tyr Cys Asn Lys Asn Thr Gly Val Cys Ile Ala Thr  
 20 25 30

&lt;210&gt; 386

&lt;211&gt; 27

&lt;212&gt; PRT

&lt;213&gt; Conus pulicarius

&lt;400&gt; 386

Glu Cys Thr Pro Pro Asp Gly Ala Cys Gly Leu Pro Thr His Cys Cys  
 1 5 10 15

Gly Phe Cys Asp Met Ala Asn Asn Arg Cys Leu  
 20 25

&lt;210&gt; 387

&lt;211&gt; 27

&lt;212&gt; PRT

&lt;213&gt; Conus pulicarius

&lt;400&gt; 387

Glu Cys Thr Pro Pro Gly Gly Ala Cys Gly Leu Pro Thr His Cys Cys  
 1 5 10 15

Gly Phe Cys Asp Met Ala Asn Asn Arg Cys Leu  
 20 25

&lt;210&gt; 388

&lt;211&gt; 28

&lt;212&gt; PRT

&lt;213&gt; Conus radiatus

&lt;400&gt; 388

His Gly Cys Lys Pro Leu Lys Arg Arg Cys Phe Asn Asp Lys Glu Cys  
 1 5 10 15

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Cys Ser Lys Phe Cys Asn Ser Val Arg Lys Gln Cys  
20 25

<210> 389  
<211> 28  
<212> PRT  
<213> Conus radiatus

<400> 389  
Arg Gly Cys Lys Pro Leu Lys Arg Arg Cys Phe Asn Asp Lys Glu Cys  
1 5 10 15

Cys Ser Lys Phe Cys Asn Ser Val Arg Asn Gln Cys  
20 25

<210> 390  
<211> 27  
<212> PRT  
<213> Conus rattus

<400> 390  
Cys Asn Ala Arg Asn Asp Gly Cys Ser Gln His Ser Gln Cys Cys Ser  
1 5 10 15

Gly Ser Cys Asn Lys Thr Ala Gly Val Cys Leu  
20 25

<210> 391  
<211> 27  
<212> PRT  
<213> Conus rattus

<400> 391  
Cys Asn Ala Arg Asn Ser Gly Cys Ser Gln His Pro Gln Cys Cys Ser  
1 5 10 15

Gly Ser Cys Asn Lys Thr Ala Gly Val Cys Leu  
20 25

<210> 392  
<211> 27  
<212> PRT  
<213> Conus rattus

<400> 392  
Cys Asn Ala Arg Asn Ser Gly Cys Ser Gln His Pro Gln Cys Cys Ser  
1 5 10 15

Gly Ser Cys Asn Lys Thr Leu Gly Val Cys Leu  
20 25

<210> 393  
<211> 34  
<212> PRT  
<213> Conus rattus

<400> 393  
Ala Cys Thr Pro Glu Gly Gly Ala Cys Ser Ser Gly Arg His Cys Cys  
1 5 10 15

Gly Phe Cys Asp Asn Val Ser His Thr Cys Tyr Gly Glu Thr Pro Ser  
20 25 30

Leu His

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<210> 394  
 <211> 36  
 <212> PRT  
 <213> Conus striatus

<400> 394  
 Ala Thr Asp Cys Ile Glu Ala Gly Asn Tyr Cys Gly Pro Thr Val Met  
 1 5 10 15  
 Lys Ile Cys Cys Gly Phe Cys Ser Pro Tyr Ser Lys Ile Cys Met Asn  
 20 25 30  
 Tyr Pro Lys Asn  
 35

<210> 395  
 <211> 26  
 <212> PRT  
 <213> Conus striatus

<400> 395  
 Cys Lys Leu Lys Gly Gln Ser Cys Arg Arg Thr Met Tyr Asp Cys Cys  
 1 5 10 15  
 Ser Gly Ser Cys Gly Arg Arg Gly Lys Cys  
 20 25

<210> 396  
 <211> 25  
 <212> PRT  
 <213> Conus striatus

<400> 396  
 Cys Lys Ala Ala Gly Lys Ser Cys Ser Arg Ile Ala Tyr Asn Cys Cys  
 1 5 10 15  
 Thr Gly Ser Cys Arg Ser Gly Lys Cys  
 20 25

<210> 397  
 <211> 26  
 <212> PRT  
 <213> Conus striatus

<400> 397  
 Cys Glu Ser Tyr Gly Lys Pro Cys Gly Ile Tyr Asn Asp Cys Cys Asn  
 1 5 10 15  
 Ala Cys Asp Pro Ala Lys Lys Thr Cys Thr  
 20 25

<210> 398  
 <211> 27  
 <212> PRT  
 <213> Conus stercusmuscarum

<400> 398  
 Cys Lys Ser Lys Gly Ala Lys Cys Ser Arg Leu Met Tyr Asp Cys Cys  
 1 5 10 15  
 Ser Gly Ser Cys Ser Gly Tyr Thr Gly Arg Cys  
 20 25

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<210> 399  
 <211> 35  
 <212> PRT  
 <213> Conus stercusmuscarum

<400> 399  
 Thr Thr Ser Cys Met Gln Ala Gly Ser Tyr Cys Gly Ser Thr Thr Arg  
 1 5 10 15  
 Ile Cys Cys Gly Tyr Cys Ala Tyr Phe Gly Lys Lys Cys Ile Asp Tyr  
 20 25 30

Pro Ser Asn  
 35

<210> 400  
 <211> 26  
 <212> PRT  
 <213> Conus stercusmuscarum

<400> 400  
 Cys Ala Ser Tyr Gly Lys Pro Cys Gly Ile Asp Asn Asp Cys Cys Asn  
 1 5 10 15

Ala Cys Asp Pro Ala Arg Asn Ile Cys Thr  
 20 25

<210> 401  
 <211> 26  
 <212> PRT  
 <213> Conus stercusmuscarum

<400> 401  
 Cys Val Ser Tyr Gly Lys Pro Cys Gly Ile Asp Asn Asp Cys Cys Asn  
 1 5 10 15

Ala Cys Asp Pro Ala Arg Asn Ile Cys Thr  
 20 25

<210> 402  
 <211> 25  
 <212> PRT  
 <213> Conus stercusmuscarum

<400> 402  
 Cys Lys Gly Lys Gly Ala Ser Cys His Lys Thr Met Tyr Asp Cys Cys  
 1 5 10 15

Ser Gly Ser Cys Thr Arg Gly Arg Cys  
 20 25

<210> 403  
 <211> 25  
 <212> PRT  
 <213> Conus striolatus

<400> 403  
 Cys Lys Gly Lys Gly Ala Ser Cys Leu Arg Thr Ala Tyr Asp Cys Cys  
 1 5 10 15

Thr Gly Ser Cys Asn Arg Gly Arg Cys  
 20 25

<210> 404  
 <211> 24

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<212> PRT  
 <213> Conus striolatus

<400> 404  
 Cys Arg Pro Ser Gly Ser Asn Cys Gly Asn Ile Ser Ile Cys Cys Gly  
 1 5 10 15

Arg Cys Val Asn Arg Arg Cys Thr  
 20

<210> 405  
 <211> 35  
 <212> PRT  
 <213> Conus striolatus

<400> 405  
~~Ser Thr Ser Cys Met Lys Ala Gly Ser Tyr Cys Val Ala Thr Thr Arg~~  
 1 5 10 15

Ile Cys Cys Gly Tyr Cys Ala Tyr Phe Gly Lys Ile Cys Ile Asp Tyr  
 20 25 30

Pro Lys Asn  
 35

<210> 406  
 <211> 28  
 <212> PRT  
 <213> Conus textile

<400> 406  
 Tyr Cys Thr Pro His Gly Gly His Cys Gly Tyr His Asn Asp Cys Cys  
 1 5 10 15

Ser His Gln Cys Asn Ile Asn Arg Asn Lys Cys Glu  
 20 25

<210> 407  
 <211> 31  
 <212> PRT  
 <213> Conus viola

<400> 407  
 Cys Ile Thr Leu Gly Thr Arg Cys Lys Val Pro Ser Gln Cys Cys Arg  
 1 5 10 15

Ser Ser Cys Lys Asn Gly Arg Cys Ala Pro Ser Pro Glu Glu Trp  
 20 25 30

<210> 408  
 <211> 25  
 <212> PRT  
 <213> Conus viola

<400> 408  
 Cys Lys Ser Arg Gly Ser Ser Cys Arg Arg Thr Ser Tyr Asp Cys Cys  
 1 5 10 15

Thr Gly Ser Cys Arg Asn Gly Lys Cys  
 20 25

<210> 409  
 <211> 36  
 <212> PRT  
 <213> Conus viola

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&lt;400&gt; 409

Ser Thr Ser Cys Met Glu Ala Arg Ser Tyr Cys Gly Pro Ala Thr Thr  
 1 5 10 15

Lys Ile Cys Cys Asp Phe Cys Ser Pro Phe Ser Asp Arg Cys Met Asn  
 20 25 30

Asn Pro Asn Asn  
 35

&lt;210&gt; 410

&lt;211&gt; 25

&lt;212&gt; PRT

&lt;213&gt; Conus viola

&lt;400&gt; 410

Cys Lys Gly Pro Gly Ala Ile Cys Ile Arg Ile Ala Tyr Asn Cys Cys  
 1 5 10 15

Lys Tyr Ser Cys Gly Asn Gly Lys Cys  
 20 25

&lt;210&gt; 411

&lt;211&gt; 28

&lt;212&gt; PRT

&lt;213&gt; Conus viola

&lt;400&gt; 411

Tyr Cys Thr Pro Tyr Gly Gly His Cys Gly Tyr Tyr Asn Asp Cys Cys  
 1 5 10 15

Ser His Gln Cys Asn Ile Asn Arg Asn Lys Cys Glu  
 20 25

&lt;210&gt; 412

&lt;211&gt; 27

&lt;212&gt; PRT

&lt;213&gt; Conus textile

&lt;400&gt; 412

Cys Thr Pro Tyr Gly Gly His Cys Gly Tyr Asn His Asp Cys Cys Ser  
 1 5 10 15

His Gln Cys Asn Ile Asn Arg Asn Lys Cys Glu  
 20 25

&lt;210&gt; 413

&lt;211&gt; 26

&lt;212&gt; PRT

&lt;213&gt; Conus tulipa

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(26)

&lt;223&gt; Xaa is Hyp

&lt;400&gt; 413

Cys Lys Ser Trp Gly Ser Xaa Cys Ser Xaa Thr Ser Thr Asn Cys Cys  
 1 5 10 15

Trp Ser Cys Ser Pro Tyr Arg Lys Lys Cys  
 20 25

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